

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Escobedo, Jaime
Quianjin, Hu
Garcia, Pablo
Williams, Lewis T.
Kothakota, Srinivas

(ii) TITLE OF THE INVENTION: Secreted Human Proteins

(iii) NUMBER OF SEQUENCES: 38

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Banner & Witcoff
(B) STREET: 1001 G Street, NW
(C) CITY: Washington
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20001

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 11-DEC-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/032757
(B) FILING DATE: 11-DEC-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kagan, Sarah A
(B) REGISTRATION NUMBER: 32141
(C) REFERENCE/DOCKET NUMBER: 2441.39505

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-508-9100
(B) TELEFAX: 202-508-9299
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2063 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTGGCA	CGAGGCCTCA	GTCTTCCAGG	GC GGCGGTGG	GTGTCCGCTT	CTCTCTGCTC	60
TTCGACTGCA	CCGCACTCGC	GC GTGACCCCT	GACTCCCCCT	AGTCAGCTCA	GC GGTGCTGC	120
CATGGCGTGG	CGGCGGCCGCG	AAGCCGGCGT	CGGGGCTCGC	GGCGTGTTGG	CTCTGGCGTT	180
GCTCGCCCTG	GCCCTGTGCG	TGCCCGGGGC	CCGGGGCCGG	GCTCTCGAGT	GGTTCTCGGC	240
CGTGGTAAAC	ATCGAGTACG	TGGACCCGCA	GACCAACCTG	ACGGTGTGGA	GC GTCTCGGA	300
GAGTGGCCGC	TT CGGCGACA	GCTCGCCCAA	GGAGGGCGCG	CATGGCCTGG	TGGGCGTCCC	360
GTGGGCGCCC	GGCGGAGACC	TCGAGGGCTG	CGCGCCCGAC	ACGCGCTTCT	TCGTGCCCGA	420
GCCC GGCGGC	CGAGGGGCCG	CGCCCTGGGT	CGCCCTGGTG	GCTCGTGGGG	GCTGCACCTT	480
CAAGGACAAG	GTGCTGGTGG	CGGCGCGGAG	GAACGCCTCG	GCCGTCGTCC	TCTACAATGA	540
GGAGCGCTAC	GGGAACATCA	CCTTGCCCAT	GTCTCACGCG	GGAACAGGAA	ATATAGTGGT	600
CATTATGATT	AGCTATCCAA	AAGGAAGAGA	AATTTGGAG	CTGGTGCAAA	AAGGAATTCC	660
AGTAACGATG	ACCATAGGGG	TTGGCACCCG	GCATGTACAG	GAGTCATCA	GC GGT CAGTC	720
TGTGGTGT	GTGGCCATTG	CCTTCATCAC	CATGATGATT	ATCTCGTTAG	CCTGGCTAAT	780
ATTTTACTAT	ATACAGCGTT	TCCTATATAAC	TGGCTCTCAG	ATTGGAAGTC	AGAGCCATAG	840
AAAAGAAACT	AAGAAAGTTA	TTGGCCAGCT	TCTACTTCAT	ACTGTAAAGC	ATGGAGAAAA	900
GGGAATTGAT	GTTGATGCTG	AAAATTGTGC	AGTGTGTATT	GAAAATTCA	AAGTAAAGGA	960
TATTATTAGA	ATTCTGCCAT	GCAAGCATAT	TTTCATAGA	ATATGCATTG	ACCCATGGCT	1020
TTTGGATCAC	CGAACATGTC	CAATGTGTAA	ACTTGATGTC	ATCAAAGCCC	TAGGATATTG	1080
GGGAGAGCCT	GGGGATGTAC	AGGAGATGCC	TGCTCCAGAA	TCTCCTCCTG	GAAGGGATCC	1140
AGCTGCAAAT	TTGAGTCTAG	CTTTACCAGA	TGATGACGGA	AGTGATGACA	GCAGTCCACC	1200
ATCAGCCTCC	CCTGCTGAAT	CTGAGCCACA	GTGTGATCCC	AGCTTTAAAG	GAGATGCAGG	1260
AGAAAATACG	GCATTGCTAG	AAGCCGGCAG	GAGTGACTCT	CGGCATGGAG	GACCCATCTC	1320
CTAGCACACG	TGCCCACTGA	AGTGGCACCA	ACAGAAGTTT	GGCTGAACT	AAAGGACATT	1380
TTATTTTTT	TACTTAGCA	CATAATTGT	ATATTGAAA	ATAATGTATA	TTATTTTACC	1440
TATTAGATT	TGATTGATA	TACAAAGGAC	TAAGATATT	TCTTCTTGAA	GAGACTTTTC	1500
GATTAGTCCT	CATATATT	TCTACTAAAA	TAGAGTGT	ACCATGAACA	GTGTGTTGCT	1560
TCAGACTATT	ACAAAGACAA	CTGGGGCAGG	TACTCTAATA	TAAAGGACAG	GTGGTGT	1620
TAAATAATTG	GCTGCTATGG	TTCTGTAAAA	ACCAGTTAAT	TCTATTTTC	AAGGTTTTG	1680
GCAAAGCACA	TCAATGTTAG	ACTAGTTGAA	GTGGAATTGT	ATAATTCAAT	TCGATAATTG	1740
ATCTCATGGG	CTTTCCCTGG	AGGAAAGGTT	TTTTTGTTG	TTTTTTTTT	AAGAACTTGA	1800
AACTTGTAAA	CTGAGATGTC	TGTAGCTTT	TTGCCCATCT	GTAGTGTATG	TGAAGATTTC	1860
AAAACCTGAG	AGCACTTTT	CTTGTTTAG	AATTATGAGA	AAGGCACTAG	ATGACTTTAG	1920
GATTTGCATT	TTTCCCTTA	TTGCCTCATT	TCTTGTGACG	CCTTGTGGG	GAGGGAAATC	1980
TGTTTATT	TTCCCTACAAA	TAAAAAGCTA	AGATTCTATA	TCGCAAAAAAA	AAAAAAAAAA	2040
AAAAAA	TTCTGCGGC	CGC				2063

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1328 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATTGGCA	CGAGGTAGGC	AAGGGATAAA	AAGGCACCTA	AGGCCCTTT	GCAATAAGAA	60
GCCAGATGGA	TAAAGGAAGT	GCTGGTCACC	CTGGAGGTGT	ACTGGTTGG	GGAAGGTCCC	120

CGGCCCCCAC	AGCCCTCTGG	GGAGCCTCAC	CCTGGCTCTC	CCCACTCACC	TCAGCCCTCA	180
GGCAGCCCC	CCACAGGGCC	CCTCTCCTGC	CTGGACAGCT	CTGCTGGTCT	CCCCGTCCCC	240
TGGAGAAGAA	CAAGGCCATG	GGTCGGCCCC	TGCTGCTGCC	CCTGCTGCTC	CTGCTGCAGC	300
CGCCAGCATT	TCTGCAGCCT	GGTGGCTCCA	CAGGATCTGG	TCCAAGCTAC	CTTTATGGGG	360
TCACTCAACC	AAAACACCTC	TCAGCCTCCA	TGGGTGGCTC	TGTGGAAATC	CCCTTCTCCT	420
TCTATTACCC	CTGGGAGTTA	GCCATAGTTC	CCAACGTGAG	AATATCCTGG	AGACGGGGCC	480
ACTTCCACGG	GCAGTCCTTC	TACAGCACAA	GGCCGCCTTC	CATTACAAG	GATTATGTGA	540
ACCGGCTCTT	TCTGAACTGG	ACAGAGGGTC	AGGAGAGCGG	CTTCCTCAGG	ATCTCAAACC	600
TGCGGAAGGA	GGACCAAGTCT	GTGTATTTCT	GCCGAGTCGA	GCTGGACACC	CGGAGATCAG	660
GGAGGCAGCA	GTTGCAGTCC	ATCAAGGGGA	CCAAACTCAC	CATCACCCAG	GCTGTCACAA	720
CCACCACAC	CTGGAGGCC	AGCAGCACAA	CCACCATAGC	CGGCCTCAGG	GTCACAGAAA	780
GCAAAGGGCA	CTCAGAATCA	TGGCACCTAA	GTCTGGACAC	TGCCATCAGG	GTTGCATTGG	840
CTGTCGCTGT	GCTCAAAACT	GTCATTTGG	GACTGCTGTG	CCTCCTCCTC	CTGTGGTGGA	900
GGAGAAGGAA	AGGTAGCAGG	GCGCCAAGCA	GTGACTTCTG	ACCAACAGAG	TGTGGGGAGA	960
AGGGATGTGT	ATTAGCCCCG	GAGGACGTGA	TGTGAGACCC	GCTTGTGAGT	CCTCCACACT	1020
CGTTCCCCAT	TGGCAAGATA	CATGGAGAGC	ACCTGAGGA	CCTTAAAAG	GCAAAGCCGC	1080
AAGGCAGAAG	GAGGCTGGGT	CCCTGAATCA	CCGACTGGAG	GAGAGTTACC	TACAAGAGCC	1140
TTCATCCAGG	AGCATCCACA	CTGCAATGAT	ATAGGAATGA	GGTCTGAACT	CCACTGAATT	1200
AAACCACCTGG	CATTGGGGGG	CTGTTTATTA	TAGCAGTGCA	AAGAGTTCT	TTATCCTCCC	1260
CAAGGATGGA	AAAATACAAT	TTATTTGCT	TACCATAAAA	AAAAAAAAAA	AAAAATTCCCT	1320
					GC GGCCGC	1328

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTGGCA	CGAGGGCAAG	ATTCGATACA	AAACCAATGA	ACCTGTGTGG	GAGGAAAAC	60
TCACTTTCTT	CATTACAAT	CCCAAGCGCC	AGGACCTTGA	AGTTGAGGTC	AGAGACGAGC	120
AGCACCACTG	TTCCCTGGGG	AACCTGAAGG	TCCCCCTCAG	CCAGCTGCTC	ACCAGTGAGG	180
ACATGACTGT	GAGCCAGCGC	TTCCAGCTCA	GTAACTCGGG	TCCAAACAGC	ACCATCAAGA	240
TGAAGATTGC	CCTGCGGGTG	CTCCATCTCG	AAAAGCGAGA	AAGGCCTCCA	GACCACCAAC	300
ACTCAGCTCA	AGTCAAACGT	CCCTCTGTGT	CCAAAGAGGG	GAGGAAAACA	TCCATCAAAT	360
CTCATATGTC	TGGGTCTCCA	GGCCCTGGTG	GCAGCAACAC	AGCTCCATCC	ACACCAGTCA	420
TTGGGGCAG	TGATAAGCCT	GGTATGGAAG	AAAAGGCCA	GCCCCCTGAG	GCCGGCCCTC	480
AGGGGCTGCA	CGACCTGGGC	AGAAGCTCCT	CCAGCCTCCT	GGCCTCCCCA	GGCCACATCT	540
CAGTCAAGGA	GCCGACCCCC	AGCATCGCCT	CGGACATCTC	GCTGCCCATC	GCCACCCAGG	600
AGCTGCGGCA	AAGGCTGAGG	CAGCTGGAAA	ACGGGACGAC	CCTGGGACAG	TCTCCACTGG	660
GGCAGATCCA	GCTGACCATC	CGGCACAGCT	CGCAGAGAAA	CAAGCTTATC	GTGGTCGTGC	720
ATGCCTGCAG	AAACCTCATT	GCCTTCTCTG	AAGACGGCTC	TGACCCCTAT	GTCCGCATGT	780
ATTATTACCA	AGACAAGAGG	CGGTCAAGGAA	GGAGGAAAAC	ACACGTGTCA	AAGAAAACAT	840
TAAATCCAGT	GTGGATCAA	AGCTTGATT	TCAGTGTTC	GTTACCAGAA	GTGCAGAGGA	900
GAACGCTCGA	CGTTGCCGTG	AAGAACAGTG	GGCCCTTCCT	GTCCAAAGAC	AAAGGGCTCC	960
TTGGCAAAGT	ATTGGTTGCT	CTGGCATTCTG	AAGAACTTGC	CAAAGGCTGG	ACCCAGTGGT	1020
ATGACCTCAC	GGAAGATGGG	ACGAGGCCTC	AGGCGATGAC	ATAGCCGCAG	CAGGCAGGAG	1080
CGTCCTCTT	CAGCGTAGCT	CTCCACCTCT	ACCCGGAACA	CACCCCTCTCA	CAGACGTACC	1140
AATGTTATTT	TTATAATTTC	ATGGATTTAG	TTATACATAC	CTTAATAGTT	TTATAAAATT	1200
GTTGACATTT	CAGGCAAATT	TGGCCAATAT	TATCATTGAA	TTTTCTGTGT	TGGATTCCT	1260
CTAGGATTTC	GCCAGTTCCCT	ACAACGTGCA	GTAGGGCGGC	GGTAGCTCTT	GTGTCTGTGG	1320
ACTCTGCTCA	GCTGTGTCCG	TAGGAGTCGG	ATGTGTCTGT	GCTTTATTAT	GGCCTTGTTT	1380
ATATATCACT	GAGGTATACT	ATGCCATGTA	AATAGACTAT	TTTTTATAAT	CTTAACATGC	1440

TGGTTAAAT	TCAGAAGGAA	ATAGATCAAG	GAAATATATA	TATTTCTTC	TAAAACATTAT	1500
TAAATTCGTG	TGACAAATAA	TCATTTCAT	CTTGGCAGCA	AAAAGTTCTC	AGTGACCTAT	1560
TTTGTGGTGT	TTCTTTGA	AAAGAAAAGC	TGAAATATTA	TTAAATGCTA	GTATGTTCT	1620
GCCCATTATG	AAAGATGAAA	TAAAGTATTC	AAAATATTAA	AAAAAAAAAA	AAAAAATTCC	1680
						1689

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTGGCA	CGAGGAGCAG	ATCTGCAAGA	GTTCGTTA	TGGAGGCTGC	TTGGGCAACA	60
AGAACAACTA	CCTTCGGAA	GAAGAGTGCA	TTCTAGCCTG	TCGGGGTGTG	CAAGGTGGC	120
CTTGAGAGG	CAGCTCTGGG	GCTCAGGCGA	CTTCCCCCA	GGGCCCTCC	ATGGAAAGGC	180
GCCATCCAGT	GTGCTCTGGC	ACCTGTCAGC	CCACCCAGTT	CCGCTGCAGC	AATGGCTGCT	240
GCATCGACAG	TTTCCTGGAG	TGTGACGACA	CCCCCAACTG	CCCCGACGCC	TCCGACGAGG	300
CTGCCTGTGA	AAAATACACG	AGTGGCTTG	ACGAGCTCCA	GCGCATCCAT	TTCCCCAGCG	360
ACAAAGGGCA	CTGCGTGGAC	CTGCCAGACA	CAGGACTCTG	CAAGGAGAGC	ATCCCGCGCT	420
GGTACTACAA	CCCCTTCAGC	GAACACTGCG	CCCGCTTAC	CTATGGTGGT	TGTTACGGCA	480
ACAAGAACAA	CTTTGAGGAA	GAGCAGCAGT	GCCTCGAGTC	TTGTCGCGGC	ATCTCCAAGA	540
AGGATGTGTT	TGGCCTGAGG	CGGGAAATCC	CCATTCCCAG	CACAGGCTCT	GTGGAGATGG	600
CTGTCGCAGT	GTTCCTGGTC	ATCTGCATTG	TGGTGGTGGT	AGCCATCTTG	GGTTACTGCT	660
TCTTCAAGAA	CCAGAGAAAG	GACTTCCACG	GACACCACCA	CCACCCACCA	CCCACCCCTG	720
CCAGCTCCAC	TGTCTCCACT	ACCGAGGACA	CGGAGCACCT	GGTCTATAAC	CACACCACGC	780
GGCCCCCTTG	AGCCTGGTC	TCACCGGCTC	TCACCTGGCC	CTGCTTCCTG	CTTGCCAAGG	840
CAGAGGCCTG	GGCTGGAAA	AACTTGGAA	CCAGACTCTT	GCCTGTTCC	CAGGCCACT	900
GTGCCTCAGA	GACCAGGGCT	CCAGCCCCCTC	TTGGAGAAGT	CTCAGCTAAG	CTCACGTCC	960
GAGAAAGCTC	AAAGGTTGG	AAGGAGCAGA	AAACCCCTGG	GCCAGAAGTA	CCAGACTAGA	1020
TGGACCTGCC	TGCATAGGAG	TTTGGAGGAA	GTTGGAGTT	TGTTTCCTCT	GTTCAAAGCT	1080
GCCTGTCCCT	ACCCCATGGT	GCTAGGAAGA	GGAGTGGGGT	GGTGTCAAGAC	CCTGGAGGCC	1140
CCAACCCTGT	CCTCCCGAGC	TCCTCTTCCA	TGCTGTGCGC	CCAGGGCTGG	GAGGAAGGAC	1200
TTCCCTGTGT	AGTTTGTGCT	GTAAAGAGTT	GCTTTTGT	TATTTAATGC	TGTGGCATGG	1260
GTGAAGAGGA	GGGGAAGAGG	CCTGTTGGC	CTCTCTATCC	TCTCTTCCTC	TTCCCCCAAG	1320
ATTGAGCTCT	CTGCCCTTGA	TCAGCCCCAC	CCTGGCCTAG	ACCAGCAGAC	AGAGCCAGGA	1380
GAAGCTCAGC	TGCATCCGC	AGCCCCCACC	CCCAAGGTT	TCCAACATCA	CAGCCCAGCC	1440
CGCCCCACTGG	GTAATAAAAG	TGGTTGTGG	AAAAAAAAAA	AAAAAAAAAA	AAGTCCTGCG	1500
						1505

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2002 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTGGCA	CGAGGGCCAT	GGCCGGGCTA	TCCCGCGGGT	CCGCGCGCGC	ACTGCTCGCC	60
GCCCTGCTGG	CGTCGACGCT	GTTGGCGCTG	CTCGTGTGCG	CCGCGCGGGG	TCGCGGCCGGC	120

CGGGACCACG	GGGACTGGGA	CGAGGCCTCC	CGGCTGCCGC	CGCTACCACC	CCGCGAGGAC	180
GCGGCGCGCG	TGGCCCGCTT	CGTGACGCAC	GTCTCCGACT	GGGGCGCTCT	GGCCACCATC	240
TCCACGCTGG	AGGCGGTGCG	CGGCCGGCCC	TTCGCCGACG	TCCTCTCGCT	CAGCGACGGG	300
CCCCCGGGCG	CGGGCAGCGG	CGTGCCCTAT	TTCTACCTGA	GCCCGCTGCA	GCTCTCCGTG	360
AGCAACCTGC	AGGAGAAATCC	ATATGCTACA	CTGACCATGA	CTTTGGCACA	GACCAACTTC	420
TGCAAGAAC	ATGGATTGTA	TCCACAAAGT	CCCCTTGTG	TTCACATAAT	GCTGTCAGGA	480
ACTGTGACCA	AGGTGAATGA	AACAGAAATG	GATATTGCAA	AGCATTGCGT	ATTCATTGCA	540
CACCCTGAGA	TGAAAACCTG	GCCTTCCAGC	CATAATTGGT	TCTTGCTAA	GTTGAATATA	600
ACCAATATCT	GGGTCTGGG	CTACTTTGGT	GGACCAAAAAA	TCGTGACACC	AGAAGAATAT	660
TATAATGTCA	CAGTTCAGTG	AAGCAGACTG	TGGTGAATT	AGCAACACTT	ATGAAGTTTC	720
TTAAAGTGGC	TCATACACAC	TTAAAAGGCT	TAATGTTCT	CTGGAAAGCG	TCCCAGAATA	780
TTAGCCAGTT	TTCTGTCACA	TGCTGGTTG	TTTGCTTGCT	TGTTTACTTG	CTTGTGTTACC	840
AATAGAGTTG	ACCTGTTATT	GGATTTCCTG	GAAGATGTGG	TAGCTACTTT	TTTCCTATT	900
TGAAGCCATT	TTCGTAGAGA	AATATCCTTC	ACTATAATCA	AATAAGTTT	GTCCCACCAA	960
TTCCAAAGAT	GTTCAGTG	GTGCTCTTG	AGAGGAATGA	GTACCAGTT	TAAATTGCC	1020
ATTGGCATT	GAAGGTAGTT	GAGTATGTGT	TCTTTATTCC	TAGAAGCCAC	TGTGCTTGTT	1080
AGAGTGCATC	ACTCACCA	GCTGCCTCTT	GAGCTGCCTG	AGCCTGGTGC	AAAAGGATTG	1140
GCCCCCATTA	TGGTGCTTCT	GAATAAAATCT	TGCCAAGATA	GACAAACAAT	GATGAAACTC	1200
AGATGGAGCT	TCCTACTCAT	GTTGATTAT	GTCTCACAAT	CCTGGGTATT	GTTAATTCAA	1260
CATAGGGTGA	AACTATTTCT	GATAAAGAAC	TTTGAAAAAA	CTTTTATAC	TCTAAAGTGA	1320
TACTCAGAAC	AAAAGAAAGT	CATAAAACTC	CTGAATTAA	TTTCCCCACC	TAAGTCGAGA	1380
CACTATTATC	AAAACACATG	TGCACACAGA	TTATTTTTG	GCTCCAAAAC	TGGATTGCAA	1440
AAGAAAGAGG	AGAGATATT	TGTGTGTTCC	TGGTATTCTT	TTATAAGTAA	AGTTACCCAG	1500
GCATGGACCA	GCTTCAGCCA	GGGACAAAT	CCCCTCCCAA	ACCACTCTCC	ACAGCTTTT	1560
AAAAATACTT	CTACTCTAA	CAATTACCTA	AGGTTCTTC	AAACCCCCC	AACTCTTAAT	1620
AGCTTCTAGT	GCTGCTACAA	TCTAAGTCAG	GTCACCAGAG	GGAAGAGAAC	ATGGCATTAA	1680
AAGAATCACA	TCTTCAGAAG	AGAAGACACT	AATATTATTA	CCCATATACA	TGATTTCAGA	1740
AGATGACATA	AGATTCTCT	TAAAGAGGAA	ATGTCAGGAA	TCAAGCCACT	GAATCCTTAA	1800
AGAGAAAAGT	TGAATATGAG	TCATTGTGTC	TGAAAACGTC	AAAGTGAAC	TAACTGAGAT	1860
CCAGCAAACA	GGTTCTGTT	AAGAAAAATA	ATTTATACTA	AATTAGTAA	AATGGACTTC	1920
TTATTCAAAG	CATCAATAAT	AAAAAGAATT	ATTTAAAAAA	AAAAAAAAAA	AAAAAAAAAA	1980
AAAAAAAAT	TCCTGCGGCC	GC				2002

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAATTCTGGCA	CGAGGGCCAC	GAECTCTGCTG	GCATTTCTTC	TATAGCCACT	GGAATCTGAT	60
CCTGATTGTC	TTCCACTACT	ACCAGGCCAT	CACCACTCCG	CCTGGGTACC	CACCCAGGG	120
CAGGAATGAT	ATCGCCACCG	TCTCCATCTG	TAAGAAGTGC	ATTTACCCCA	AGCCAGCCCG	180
AACACACCAC	TGCAGCATCT	GCAACAGGTG	TGTGCTGAAG	ATGGATCACC	ACTGCCCTG	240
GCTAAACAAT	TGTGTGGGCC	ACTATAACCA	TCGGTACTTC	TTCTCTTTCT	GCTTTTCAT	300
GAECTCTGGC	TGTGTCTACT	GCAGCTATGG	AAGTTGGGAC	CTTTTCCGGG	AGGCTTATGC	360
TGCCATTGAG	AAAATGAAAC	AGCTCGACAA	GAACAAACTA	CAGGCGGTTG	CCAACCAGAC	420
TTATCACCAG	ACCCCACCA	CCACCTTCTC	CTTTCGAGAA	AGGATGACTC	ACAAGAGTCT	480
TGTCTACCTC	TGGTTCTGT	GCAGTTCTGT	GGCACTTGCC	CTGGGTGCC	TAACTGTATG	540
GCATGCTGTT	CTCATCAGTC	GAGGTGAGAC	TAGCATCGAA	AGGCACATCA	ACAAGAAGGA	600
GAGACGTCGG	CTACAGGCCA	AGGGCAGAGT	ATTAGGAAT	CCTTACAAC	ACGGCTGCTT	660
GGACAACTGG	AAGGTATTCC	TGGGTGTGGA	TACAGGAAGG	CACTGGCTTA	CTCGGGTGCT	720
CTTACCTTCT	ACTCACTTGC	CCCATGGGAA	TGGAATGAGC	TGGGAGCCCC	CTCCCTGGGT	780

GACTGCTCAC	TCAGCCTCTG	TGATGGCAGT	GTGAGCTGGA	CTGTGTCAGC	CACGACTCGA	840
GCACTCATTC	TGCTCCCTAT	GTTATTCAA	GGGCCTCCAA	GGGCAGCTTT	TCTCAGAACATC	900
CTTGATCAA	AAGAGCCAGT	GGGCCTGCCT	TAGGGTACCA	TGCAGGACAA	TTCAAGGACC	960
AGCCTTTTA	CCACTGCAGA	AGAAAGACAC	AATGTGGAGA	AATCTTAGGA	CTGACATCCC	1020
TTTACTCAGG	CAAACAGAAG	TTCCAACCCC	AGACTAGGGG	TCAGGCAGCT	AGCTACCTAC	1080
CTTGCCCAGT	GCTGACCCGG	ACCTCCTCCA	GGATACAGCA	CTGGAGTTGG	CCACCACCTC	1140
TTCTACTTGC	TGTCTGAAAAA	AACACCTGAC	TAGTACAGCT	GAGATCTTGG	CTTCTCAACA	1200
GGGCAAAGAT	ACCAGGCCTG	CTGCTGAGGT	CACTGCCACT	TCTCACATGC	TGCTTAAGGG	1260
AGCACAAATA	AAGGTATTG	ATTTTAAAAA	AAAAAAAAAA	AAAAAAAAAT	TCCTGCAGGCC	1320
GC						1322

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAATTGGCA	CGAGGAGCCT	GCCTTCATCT	AGGATGGCTC	CTCTGGCAT	GCTGCTTGGG	60
CTGCTGATGG	CCGCCTGCTT	CACCTCTGC	CTCAGTCATC	AGAACCTGAA	GGAGTTTGCC	120
CTGACCAACC	CAGAGAAGAG	CAGCACCAAA	GAAACAGAGA	GAAAAGAAAC	CAAAGCCGAG	180
GAGGAGCTGG	ATGCCGAAGT	CCTGGAGGTG	TTCCACCCGA	CGCATGAGTG	GCAGGCCCTT	240
CAGCCAGGGC	AGGCTGTCCC	TGCAGGATCC	CACGTACGGC	TGAATCTTCA	GACTGGGGAA	300
AGAGAGGCAA	AACTCCAATA	TGAGGACAAG	TTCCGAAATA	ATTTGAAAGG	CAAAAGGCTG	360
GATATCAACA	CCAACACCTA	CACATCTCAG	GATCTCAAGA	GTGCACTGGC	AAAATTCAAG	420
GAGGGGGCAG	AGATGGAGAG	TTCAAAGGAA	GACAAGGCAA	GGCAGGCTGA	GGTAAAGCGG	480
CTCTTCCGCC	CCATTGAGGA	ACTGAAGAAA	GACTTGATG	AGCTGAATGT	TGTCATTGAG	540
ACTGACATGC	AGATCATGGT	ACGGCTGATC	AACAAGTTCA	ATAGTTCCAG	CTCCAGTTG	600
GAAGAGAAGA	TTGCTGCGCT	CTTGATCTT	GAATATTATG	TCCATCAGAT	GGACAATGCG	660
CAGGACCTGC	TTTCCTTGG	TGGTCTTCAA	GTGGTGATCA	ATGGGCTGAA	CAGCACAGAG	720
CCCCTCGTGA	AGGAGTATGC	TGCGTTGTG	CTGGCGCTG	CCTTTCCAG	CAACCCCAAG	780
GTCCAGGTGG	AGGCCATCGA	AGGGGGAGCC	CTGCAGAACG	TGCTGGTCAT	CCTGGCCACG	840
GAGCAGCCGC	TCACTGCAAA	GAAGAAGGTC	CTGTTGCAC	TGTGCTCCCT	GCTGCGCCAC	900
TTCCCCCTATG	CCCAGCGGCA	GTT CCTGAAG	CTCGGGGGC	TGCAGGTCCCT	GAGGACCTG	960
GTGCAGGAGA	AGGGCACCGA	GGT GCTCGCC	GTGCGCGTGG	TCACACTGCT	CTACGACCTG	1020
GTCACGGAGA	AGATGTTCGC	CGAGGAGGAG	GCTGAGCTGA	CCCAGGAGAT	GTCCCCAGAG	1080
AAGCTGCAGC	AGTATCGCCA	GGTACACCTC	CTGCCAGGCC	TGTGGAAACA	GGGCTGGTGC	1140
GAGATCACGG	CCCACCTCCT	GGCGCTGCC	GAGCATGATG	CCC GTGAGAA	GGT GCTGCAG	1200
ACACTGGCG	TCCTCCTGAC	CACCTGCCGG	GACCGCTACC	GTCAGGACCC	CCAGCTCGGC	1260
AGGACACTGG	CCAGCCTGCA	GGCTGAGTAC	CAGGTGCTGG	CCAGCCTGGA	GCTGCAGGAT	1320
GGTGAGGACG	AGGGCTACTT	CCAGGAGCTG	CTGGGCTCTG	TCAACAGCTT	GCTGAAGGAG	1380
CTGAGATGAG	GCCCCACACC	AGGACTGGAC	TGGGATGCCG	CTAGTGAGGC	TGAGGGGTGC	1440
CAGCGTGGGT	GGGCTTCTCA	GGCAGGAGGA	CATCTTGGCA	GTGCTGGCTT	GGCCATTAAA	1500
TGGAAACCTG	AAGGCCAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	1560
TTCCTGCGGC	CGC					1573

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAATTCTGGCA	CGAGGGGGCT	TTAAGGGACA	GCTGAGCCGG	CAGGTGGCAG	ATCAGATGTG	60
GCAGGCTGGG	AAAAGACAAG	CCTCCAGGGC	CTTCAGCTT	TACGCCAAC	TCGACATCCT	120
CAGACCCTAC	TTTGATGTGG	AGCCTGCTCA	GGTGCAGAAGC	AGGCTCCTGG	AGTCCATGAT	180
CCCTATCAAG	ATGGTCAACT	TCCCCCAGAA	AATTGCAGGT	GAACCTCTATG	GACCTCTCAT	240
GCTGGTCTTC	ACTCTGGTTG	CTATCCTACT	CCATGGGATG	AAGACGTCTG	ACACTATTAT	300
CCGGGAGGGC	ACCCTGATGG	GCACAGCCAT	TGGCACCTGC	TTCGGCTACT	GGCTGGGAGT	360
CTCATCCTTC	ATTTACTTCC	TTGCCTACCT	GTGCAACGCC	CAGATCACCA	TGCTGCAGAT	420
GTTGGCACTG	CTGGGCTATG	GCCTCTTGG	GCATTGCATT	GTCCTGTTCA	TCACCTATAA	480
TATCCACCTC	CACGCCCTCT	TCTACCTCTT	CTGGCTGTTG	GTGGGTGGAC	TGTCCACACT	540
GCGCATGGTA	GCAGTGTGTTG	TGTCTCGGAC	CGTGGGCC	ACACAGCGGC	TGCTCCTCTG	600
TGGCACCCCTG	GCTGCCCTAC	ACATGCTCTT	CCTGCTCTAT	CTGCATTTG	CCTACCACAA	660
AGTGGTAGAG	GGGATCCTGG	ACACACTGGA	GGGCC	ATCCC	TCCAGAGGGT	720
CCCCAGAGAC	ATCCCTGCCA	TGCTCCCTGC	TGCTCGGCTT	CCCACCACCG	TCCTCAACGC	780
CACAGCCAAA	GCTGTTGCGG	TGACCCCTGCA	GTCACACTGA	CCCCACCTGA	AATTCTTGGC	840
CAGTCCTCTT	TCCCGCAGCT	GCAGAGAGGA	GGAAGACTAT	TAAAGGACAG	TCCTGATGAC	900
ATGTTTCGTA	GATGGGGTTT	GCAGCTGCCA	CTGAGCTGTA	GCTGCGTAAG	TACCTCCTTG	960
ATGCCTGTCG	GCACTTCTGA	AAGGCACAAG	GCCAAGAACT	CCTGCCAGG	ACTGCAAGGC	1020
TCTGCAGCCA	ATGCAGAAAAA	TGGTCAGCT	CCTTGAGAA	CCCCTCCCCA	CCTACCCCTT	1080
CCTTCCTCTT	TATCTCTCCC	ACATTGTCTT	GCTAAATATA	GACTGGTAA	TTAAAATGTT	1140
GATTGAAGTC	TGGAAAAAAA	AAAAAAAAAA	AATTCCCTGCG	GCCGC		1185

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1226 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTCTGGCA	CGAGGCAAGC	CACCATCTTC	CTTCGGCCTG	CACCCCTTA	AAGGCACCCA	60
GACCCCTCTG	GAAAAAAGATG	AACTGAAGCC	CTTGACATC	CTCCAGCCTA	AGGAGTACTT	120
CCAGCTCAGC	CGCCACACGG	TCATTAAGAT	GGGAAGTGAG	AACGAGGCC	TGGATCTCTC	180
CATGAAGTCA	GTGCCCTGGC	TCAAGGCTGG	TGAAGTCAGT	CCCCAATCT	TCCAGGAAGA	240
TGCAGCCCTA	GACCTGTCAG	TGGCAGCCCA	CCGGAAATCC	GAGCCTCCCC	CTGAGACACT	300
GTATGACAGT	GGTGCATCAG	TGGACAGCTC	AGGTACACACA	GTGATGGAGA	AACTCCAG	360
TGGCATGGAA	ATTCTTTG	CCCCTGCCAC	GTCCCATGAG	GCCCCAGCCA	TGATGGATAG	420
TCACATCAGC	AGCAGTGATG	CTGCTACCGA	GATGCTCAGC	CAGCCCAACC	ACCCCAGCGG	480
CGAAGTCAAG	GCTGAAAATA	ACATTGAGAT	GGTGGCGAG	TCCCAGGC	CCAAGGTCA	540
TGTCTCTGTC	GAAGATGCTG	TGCCTACCAT	ATTCTGTGGC	AAGATCAAAG	GCCTCTCAGG	600
GGTGTCCACC	AAAAACTTCT	CCTTCAAAAG	AGAAGACTCC	GTGCTTCAGG	GCTATGACAT	660
CAACAGCCAA	GGGGAAGAGT	CCATGGAAA	TGCAGAGCCC	CTTAGGAAAC	CCATCAAAAA	720
CCGGAGCATA	AAGTTAAAGA	AAGTGAAC	CCAGGAAGTA	CACATGCTCC	CAATCAAAAA	780
ACAACGGCTG	GCCACCTTT	TTCCAAGAAA	GTAAATAACG	GCTTTTAAA	ATTGTATGA	840
TTATAATATG	GGGAAAGGTG	CATTGGTTT	ATAAAAAGGC	ATTTAAAACA	AATTATCTTT	900
GTTAATTATT	TTGGGGAGTA	GTTGGAAAT	GGAAAGGTGA	ATTGGCTCTA	GAGGCCCTGT	960
ATGCTAGTAT	CATTTCTT	TTAATT	GACTTTAC	AAATGAGTAA	ATAAGAGCAA	1020
CCTATTCTTC	AAGCAGATTG	CACATT	GCAGCTTAA	TGGAATATTG	GGTGAATTAG	1080
AGGGTAAAAA	AAAGCTATT	TCATTGCCAC	AAAGTCTT	GATGATGTAA	TACCTAATAA	1140
AGGGTAGGAT	GAATATTCA	CAATAATGT	TTGTTGCAC	TAAAAAAA	AAAAAAA	1200
AAAAAAA	AAATTCC	GGCGC				1226

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1049 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAATTCTGGCA	CGAGGGCGCC	ATGGTGAAGG	TGACGTTCAA	CTCCGCTCTG	GCCCAGAAGG	60
AGGCCAAGAA	GGACGAGCCC	AAGAGCGGCG	AGGAGGCGCT	CATCATCCCC	CCCGACGCCG	120
TCGCGGTGGA	CTGCAAGGAC	CCAGATGATG	TGGTACCAAGT	TGGCCAAAGA	AGAGCCTGGT	180
GTTGGTGCAT	GTGCTTGGA	CTAGCATTAA	TGCTTGCAGG	TGTTATTCTA	GGAGGGAGCAT	240
ACTTGTACAA	ATATTTGCA	CTTCAACCAG	ATGACGTGTA	CTACTGTGGA	ATAAAAGTACA	300
TCAAAGATGA	TGTCATCTTA	AATGAGCCCT	CTGCAGATGC	CCCAGCTGCT	CTCTACCAGA	360
CAATTGAAGA	AAATATTAAA	ATCTTGAAG	AAGAAGAAGT	TGAATTTATC	AGTGTGCCTG	420
TCCCAGAGTT	TGCAGATAGT	GATCCTGCCA	ACATTGTTCA	TGACTTTAAC	AAGAAAACCTA	480
CAGCCTATT	AGATCTTAAC	CTGGATAAGT	GCTATGTGAT	CCCTCTGAAC	ACTTCCATTG	540
TTATGCCACC	CAGAAACCTA	CTGGAGTTAC	TTATTAACAT	CAAGGCTGGA	ACCTATTGTC	600
CTCAGTCCTA	TCTGATTCAT	GAGCACATGG	TTATTACTGA	TCGCATTGAA	AACATTGATC	660
ACCTGGGTTT	CTTTATT	CGACTGTGTC	ATGACAAGGA	AACTACAAA	CTGCAACGCA	720
GAGAAACTAT	TAAAGGTATT	CAGAAACGTG	AAGCCAGCAA	TTGTTTCGCA	ATTCCGGCATT	780
TTGAAAACAA	ATTTGCCGTG	GAAACTTAA	TTTGTTCCTG	AACAGTCAAG	AAAAACATTA	840
TTGAGGAAAA	TTAATATCAC	AGCATAACCC	CACCCTTAC	ATTTGTTGC	AGTTGATTAT	900
TTTTTAAAGT	CTTCTTCAT	GTAAGTAGCA	AACAGGGCTT	TACTATCTT	TCATCTCATT	960
AATTCAATT	AAACCATTAC	CTTAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	1020
		AAAAAAATTCC	TGCGGCCGC			1049

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAATTCTGGCA	CGAGGGGAGA	ATACTTTTG	CGATGCCTAC	TGGAGACTTT	GATTCGAAGC	60
CCAGTTGGGC	CGACCAGGTG	GAGGAGGAGG	GGGAGGACGA	CAAATGTGTC	ACCAGCGAGC	120
TCCTCAAGGG	GATCCCTCTG	GCCACAGGTG	ACACCAGCCC	AGAGCCAGAG	CTACTGCCGG	180
GAGCTCCACT	GCCGCTCCC	AAGGAGGTCA	TCAACGGAAA	CATAAAGACA	GTGACAGAGT	240
ACAAGATAGA	TGAGGATGGC	AAGAAGTTCA	AGATTGTCCG	CACCTTCAGG	ATTGAGACCC	300
CCAAGGCTTC	AAAGGCTGTC	GCAAGGAGGA	AGAACTGGAA	GAAGTTCGGG	AACTCAGAGT	360
TTGACCCCCC	CGGACCAAT	GTGCCACCA	CCACTGTCA	TGACGATGTC	TCTATGACGT	420
TCATCACCAG	CAAAGAGGAC	CTGAAC TGCC	AGGAGGAGGA	GGACCCATG	AACAAATTCA	480
AGGGCCAGAA	GATCGTGTCC	TGCCGCATCT	GCAAGGGCGA	CCACTGGACC	ACCCGCTGCC	540
CCTACAAGGA	TACGCTGGGG	CCCATGCAGA	AGGAGCTGGC	CGAGCAGCTG	GGCCTGTCTA	600
CTGGCGAGAA	GGAGAAAGCTG	CCGGGAGAGC	TAGAGCCGGT	GCAGGCCACG	CAGAACAGA	660
CAGGGAAGTA	TGTGCCGCCG	AGCCTGCGCG	ACGGGGCCAG	CCGCCGCCGG	GAGTCCATGC	720
AGCCCAACCG	CAGAGCCGAC	GACAACGCCA	CCATCCGTGT	CACCAACTTG	CGCAGAGGAC	780
ACGCGTGAGA	CCGACCTGCA	GGAGCTCTTC	CGGCCTTTCG	GCTCCATCTC	CCGCATCTAC	840
CTGGCTAAGG	ACAAGACCAC	TGGCCAATCC	AAGGGCTTG	CCTTCATCAG	CTTCCACCGC	900

CGCGAGGGATG	CTGCGCGTGC	CATTGCCGGG	GTGTCCGGCT	TTGGCTACGA	CCACCTCATC	960
CTCAACGTCG	AGTGGGCCAA	GCCGTCCACC	AACTAAGCCA	GCTGCCACTG	TGTACTCGGT	1020
CCGGGACCCCT	TGGCGACAGA	AGACAGCCTC	CGAGAGCGCG	GGCTCCAAGG	GCAATAAAGC	1080
AGCTCCACTC	TCAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAT	TCCTGCAGGCC	1140
GC						1142

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAATTCCGGCA	CGAGGGAAAC	ATGGCGGTAG	GCTGGGACCA	TAACACAAGC	ATGACTATAT	60
GAAGGAAGAG	GAAGGTTTTC	CTGAAGATGA	GGCGACTGAA	TCGGAAAAAA	ACTTTAAGTT	120
TGGTAAAAGA	GTTGGATGCC	TTTCCGAAGG	TTCCTGAGAG	CTATGTAGAG	ACTTCAGCCA	180
GTGGAGGTAC	AGTTTCTCTA	ATAGCATTAA	CAACTATGGC	TTTATTAACC	ATAATGGAAT	240
TCTCAGTATA	TCAAGATACA	TGGATGAAGT	ATGAATACGA	AGTAGACAAG	GATTTTCTA	300
GCAAATTAAG	AATTAATATA	GATATTACTG	TTGCCATGAA	GTGTCAATAT	GTTGGAGCGG	360
ATGTATTGGA	TTTAGCAGAA	ACAATGGTTG	CATCTGCAGA	TGGTTTAGTT	TATGAACCAA	420
CAGTATTGAA	TCTTCACCA	CAGCAGAAAG	AGTGGCAGAG	GATGCTGCAG	CTGATTCAA	480
GTAGGCTACA	AGAAGAGCAT	TCACTTCAAG	ATGTGATATT	AAAAGTGCT	TTTAAAAGTA	540
CATCAACAGC	TCTTCCACCA	AGAGAAGATG	ATTCATCACA	GTCTCCAAAT	GCATGCAGAA	600
TTCATGGCCA	TCTATATGTC	AATAAAGTAG	CAGGAAATT	TCACATAACA	GTGGGCAAGG	660
CAATTCCACA	TCCTCGTGGT	CATGCACATT	TGGCAGCACT	TGTCAACCAT	GAATCTTACA	720
ATTTTCTCA	TAGAATAGAT	CATTTGTCTT	TTGGAGAGCT	TGTTCCAGCA	ATTATTAATC	780
CTTTAGATGG	AACTGAAAAA	ATTGCTATAG	ATCACAACCA	GATGTTCCAA	TATTTTATTA	840
CAGTTGTGCC	AACAAAACCA	CATACATATA	AAATATCAGC	AGACACCCAT	CAGTTTCTG	900
TGACAGAAAG	GGAACGTATC	ATTAACCATG	CTGCAGGCAG	CCATGGAGTC	TCTGGGATAT	960
TTATGAAATA	TGATCTCAGT	TCTCTTATGG	TGACAGTTAC	TGAGGGAGCAC	ATGCCATTCT	1020
GGCAGTTTT	TGTAAGACTC	TGTGGTATTG	TTGGAGGAAT	CTTTCAACA	ACAGGCATGT	1080
TACATGGAAT	TGGAAAATT	ATAGTTGAAA	TAATTGCTG	TCGTTTCAGA	CTTGGATCCT	1140
ATAAACCTGT	CAATTCTGTT	CCTTTGAGG	ATGGCCACAC	AGACAACCAC	TTACCTCTT	1200
TAGAAAATAA	TACACATTAA	CACCTCCCAG	TTGAAGGAGA	AAAACCTTT	GCCTGAGACA	1260
AAAAACCTTT	TTTTAATAAT	AAAATATTGT	GCAATATATT	CAAAGAAAAG	AAAACACAAA	1320
TAAGCAGAAA	ACATACTTAT	TTTAAAAAAG	AAAAAAAAGG	ATAAAAAAAC	CCAAACTGAA	1380
ATTCTATATA	CGTTGTGTCT	GTTACAAATG	TCGTAGAAGA	AATCATGCAG	CTAAACGATG	1440
AAGAAGCCCC	ACTGGAGTGT	TGCTTGAAAG	ATGACGCCTT	CTTATATTTT	CATAGCAAAT	1500
GGGTGGTATC	AAAATCAGAC	ATTGCTTCTT	GCTGATAAAA	AGCCTGAAGG	AAATAAGTGA	1560
AACTACATCT	ATGGGAAAAA	AAAAAACATT	GAGAAGTGCA	AATGTTCGCA	TCCTTTGTT	1620
TTTAAAAGAT	ATGATGTCAG	AATAAAATGT	GGAAAACATA	CGGAAAAAAA	AAAAAAA	1680
AAATTCCCTGC	GGCCGC					1696

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAATTGGCA	CGAGGGCGCA	CGAGGGCGCA	CGAGGGTGGC	ATATCACGGC	CATGGGTCT	60
CAGCATTCCG	CTGCTGCTG	CCCCTCCTCC	TGCAGGCGAA	AGCAAGAAGA	TGACAGGGAC	120
GGTTTGCTGG	CTGAACGAGA	GCAGGAAGAA	GCCATTGCTC	AGTTCCCATA	TGTGGAATT	180
ACCGGGAGAG	ATAGCATCAC	CTGTCTCACG	TGCCAGGGGA	CAGGCTACAT	TCCAACAGAG	240
CAAGTAAATG	AGTTGGTGGC	TTTGATCCC	CACAGTGATC	AGAGATTGCG	CCCTCAGCGA	300
ACTAAGCAAT	ATGTCCTCCT	GTCCATCCTG	CTTTGTCTCC	TGGCATCTGG	TTTGGTGGTT	360
TTCTTCCTGT	TTCCGCATT	AGTCCTTGTG	GATGATGACG	GCATCAAAGT	GGTGAAAGTC	420
ACATTTAATA	AGCAAGACTC	CCTTGTAAATT	CTCACCATCA	TGGCCACCCT	GAAAATCAGG	480
AACTCCAAC	TCTACACGGT	GGCAGTGACC	AGCCTGTCCA	GCCAGATTCA	GTACATGAAC	540
ACAGTGGTCA	GTACATATGT	GAECTACTAAC	GTCTCCCTTA	TTCCACCTCG	GAGTGAGCAA	600
CTGGTGAATT	TTACCGGGAA	GGCCGAGATG	GGAGGACCGT	TTTCCTATGT	GTACTTCTTC	660
TGCACGGTAC	CTGAGATCCT	GGTGCACAAC	ATAGTGATCT	TCATGCGAAC	TTCACTGAAG	720
ATTCATACA	TTGGCCTCAT	GACCCAGAGC	TCCTTGGAGA	CACATCACTA	TGTGGATTGT	780
GGAGGAAATT	CCACAGCTAT	TTAACAACTG	CTATTGGTTC	TTCCACACAG	CGCCTGTAGA	840
AGAGAGCACA	GCATATGTT	CCAAGGCCTG	AGTTCTGGAC	CTACCCCCAC	GTGGTGTAAAG	900
CAGAGGAGGA	ATTGGGTCAC	TTAACTCCC	GCAAACATCC	TCCTGCCACT	TAGGAGGAAA	960
CACCTCCCTA	TGGTACCAATT	TATGTTCTC	AGAACCAAGCA	GAATCAGTGC	CTAGCCTGTG	1020
CCCAGCAAAT	AGTTGGCACT	CAATAAAGAT	TTGCAGAATT	TAAAAA	A	1080
AAAAAAATTC	CTGCGGCCGC					1100

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAATTGGCA	CGAGGGTACC	TGCTTTCTA	TTGCCTCTT	GAAACAATGG	TCACGTGTT	60
CCATGTTCCC	TACTCGGCTC	TCACCATGTT	CATCAGCACC	GAGCAGACTG	AGCGGGATT	120
TGCCACCGCC	TATCGGATGA	CTGTGGAAGT	GCTGGGCACA	GTGCTGGCA	CGGCGATCCA	180
GGGACAAATC	GTGGGCCAAG	CAGACACGCC	TTGTTCCAG	GACCTCAATA	GCTCTACAGT	240
AGCTTCACAA	AGTGCCAAC	ATACACATGG	CACCACTCA	CACAGGGAAA	CGCAAAAGGC	300
ATACCTGCTG	GCAGCGGGGG	TCATTGTCTG	TATCTATATA	ATCTGTGCTG	TCATCCTGAT	360
CCTGGCGTG	CGGGAGCAGA	GAGAACCTA	TGAAGCCCAG	CAGTCTGAGC	CAATCGCCTA	420
CTTCCGGGGC	CTACGGCTGG	TCATGAGCCA	CGGCCCATAC	ATCAAACCTA	TTACTGGCTT	480
CCTCTTCACC	TCCTTGGCTT	TCATGCTGGT	GGAGGGGAAC	TTTGTCTTGT	TTTGCACCTA	540
CACCTGGGC	TTCCGCAATG	AATTCCAGAA	TCTACTCCTG	GCCATCATGC	TCTCGGCCAC	600
TTTAACCATT	CCCATCTGGC	AGTGGTTCTT	GACCCGGTT	GGCAAGAAGA	CAGCTGTATA	660
TGTTGGGATC	TCATCAGCAG	TGCCATTCT	CATCTTGGTG	GCCCTCATGG	AGAGTAACCT	720
CATCATTACA	TATGCGGTAG	CTGTGGCAGC	TGGCATCAGT	GTGGCAGCTG	CCTTCTTACT	780
ACCCCTGGTCC	ATGCTGCCTG	ATGTATTGA	CGACTTCCAT	CTGAAGCAGC	CCCACCTCCA	840
TGGAACCGAG	CCCATCTTCT	TCTCCTCTA	TGTCTTCTTC	ACCAAGTTG	CCTCTGGAGT	900
GTCACTGGGC	ATTCTACCC	TCAGTCTGGA	CTTGCAAGGG	TACCAGACCC	GTGGCTGCTC	960
GCAGCCGGAA	CGTGTCAAGT	TTACACTGAA	CATGCTCGTG	ACCATGGCTC	CCATAGTTCT	1020
CATCCTGCTG	GGCCTGCTGC	TCTTCAAAT	GTACCCATT	GATGAGGAGA	GGCGGCCGGCA	1080
GAATAAGAAG	GCCCTGCAGG	CACTGAGGGA	CGAGGCCAGC	AGCTCTGGCT	GCTCAGAAAC	1140
AGACTCCACA	GAGCTGGCTA	GCATCCTCTA	GGGCCGCCA	CGTTGCCCGA	AGCCACCATG	1200
CAGAAGGCCA	CAGAAGGGAT	CAGGACCTGT	CTGCCGGCTT	GCTGAGCAGC	TGGACTGCAG	1260
GTGCTAGGAA	GGGAAGTGA	GAATCAAGGA	GGTGGCCAG	GACACTTGCT	GTGCTCACTG	1320
TGGGGCCGGC	TGCTCTGTGG	CCTCCTGCCT	CCCCCTCTGCC	TGCCTGTGGG	GCCAAGCCCT	1380
GGGGCTGCCA	CTGTGAATAT	GCCAAGGACT	GATCGGGCCT	AGCCCGGAAC	ACTAATGTAG	1440
AAACCTTTT	TTTACAGAGC	CTAATTAATA	ACTTAATGAC	TGTGTACATA	GCAATGTGTG	1500

TGTATGTATA TGTCTGTGAG CTATTAATGT TATTAATTTCATAAAAGCT GGAAAGCAAA	1560
AAAAAAAAAAA AAAAATTCCGC	1588

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTGGCGA CGAGGGCGGAA GTCCCGTCTC ACGGTTGCCCG TGGCAGCGCG CGAGGCTGGT	60
GAGTCGGCAG CCCTGTGGCA GCCGGCGGGC TGGTTTCCAT GGTTGCACGA TTAGGAACCA	120
CCAGCTGCTG CATCCCAGTGG CCAGGGGTGG CGTCCAGGTG GCAGAGCAGC TAGGAACGCA	180
AGGCCTGAAC CTGGGGCCAG ACACCCTGCT CTCCCAGGCA TGGTCAACGA CCCTCCAGTA	240
CCTGCCTTAC TGTGGGCCA GGAGGTGGGC CAAGTCTTGG CAGGCCGTGC CCGCAGGCTG	300
CTGCTGCAGT TTGGGGTGCT CTTCTGCACC ATCCTCCTT TGCTCTGGGT GTCTGTCTTC	360
CTCTATGGCT CCTTCTACTA TTCCTATATG CCGACAGTCA GCCACCTCAG CCCTGTGCAT	420
TTCTACTACA GGACCGACTG TGATTCCCTCC ACCACCTCAC TCTGCTCCTT CCCTGTTGCC	480
AATGTCTCGC TGACTAACAGG TGGACGTGAT CGGGTGCTGA TGTATGGACA GCCGTATCGT	540
GTTACCTTAG AGCTTGAGCT GCCAGAGTCC CCTGTGAATC AAGATTGGGG CATGTTCTTG	600
GTCACCATT CCTGCTACAC CAGAGGTGGC CGAACATCATCT CCACCTCTTC GCGTTGGTG	660
ATGCTGCATT ACCGCTCAGA CCTGCTCCAG ATGCTGGACA CACTGGTCTT CTCTAGCCTC	720
CTGCTATTTG GCTTGCAGA GCAGAACAGC CTGCTGGAGG TGGAACCTCA CGCAGACTAT	780
AGAGAGAACT CGTACGTGCC GACCACTGGA GCGATCATTG AGATCCACAG CAAGCGCATT	840
CAGCTGTATG GAGCCTACCT CCGCATCCAC GCGCACTTCA CTGGGCTCAG ATACCTGCTA	900
TACAACCTCC CGATGACCTG CGCCTTCATA GGTGTTGCCA GCAACTTCAC CTTCCCTCAGC	960
GTCATCGTGC TCTTCAGCTA CATGCAGTGG GTGTGGGGGG GCATCTGGCC CCGACACCGC	1020
TTCTCTTGC AGGTTAACAT CCGAAAAAGA GACAATTCCC GGAAGGAAGT CCAACGAAGG	1080
ATCTCTGCTC ATCAGGCCAGG GCCTGAAGGC CAGGAGGAGT CAACTCCGCA ATCAGATGTT	1140
ACAGAGGATG GTGAGAGCCC TGAAGATCCC TCAGGGACAG AGGTCACTG TCCGAGGAGG	1200
AGAAACCAGA TCAGCAGCCC CTGAGCGGAG AAGAGGAGCT AGAGCCTGAG GCCAGTGATG	1260
GTTCAGGCTC CTGGGAAGAT GCAGCTTGC TGACGGAGGC CAACCTGCCT GCTCCTGCTC	1320
CTGCTTCTGC TTCTGCCCT GTCCTAGAGA CTCTGGGCAG CTCTGAACCT GCTGGGGGTG	1380
CTCTCCGACA GCGCCCCACC TGCTCTAGTT CCTGAAGAAA AGGGGCAGAC TCCTCACATT	1440
CCAGCACTTT CCCACCTGAC TCCTCTCCCC TCGTTTTCC TTCAATAAAC TATTTGTGT	1500
CAAAAAAAAAA AAAAAAAAAA AATTCCGTGCG GCCGC	1535

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAATTGGCGA CGAGGGCGGG CGCTACGGGC TTGACTCCCC CAAGGCCGAG GTCCGGGCC	60
AGGTGCTGGC GCCGCTGCCCT CTCCACGGAG TTGCTGATCA TCTGGCTGT GATCCACAAA	120
CCCGGTTCTT TGTCCCTCCT AATATCAAAC AGTGGATTGC CTTGCTGCAG AGGGGAAACT	180
GCACGTTAA AGAGAAAATA TCACGGGCCG CTTTCCACAA TGCAGTTGCT GTAGTCATCT	240
ACAATAATAA ATCCAAAGAG GAGCCAGTTA CCATGACTCA TCCAGGCAGT GGAGATATTA	300

TTGCTGTCAT	GATAACAGAA	TTGAGGGGTA	AGGATATT	TGAGTTATCTG	GAGAAAAACA	360
TCTCTGTACA	AATGACAATA	GCTGTTGGAA	CTCGAATGCC	ACCGAAGAAC	TTCAGCCGTG	420
GCTCTCTAGT	CTTCGTGTCA	ATATCCTTA	TTGTTTGAT	GATTATTCT	TCAGCATGGC	480
TCATATTCTA	CTTCATTCAA	AAGATCAGGT	ACACAAATGC	ACGCGACAGG	AACCAGCGTC	540
GTCTCGGAGA	TGCAGCCAAG	AAAGCCATCA	GTAAATTGAC	AACCAGGACA	GTAAAGAAGG	600
GTGACAAGGA	AACTGACCCA	GACTTGATC	ATTGTGCAGT	CTGCATAGAG	AGCTATAAGC	660
AGAATGATGT	CGTCCGAATT	CTCCCCTGCA	AGCATGTTT	CCACAAATCC	TGCGTGGATC	720
CCTGGCTTAG	TGAACATTGT	ACCTGTCCTA	TGTGCAAAC	TAATATATTG	AAGGCCCTGG	780
GAATTGTGCC	GAATTGCCA	TGTACTGATA	ACGTAGCATT	CGATATGGAA	AGGCTCACCA	840
GAACCCAAGC	TGTTAACCGA	AGATCAGCCC	TCGGCGACCT	CGCCGGCGAC	AACTCCCTTG	900
GCCTTGAGCC	ACTTCGAACT	TCGGGGATCT	CACCTCTTCC	TCAGGATGGG	GAGCTCACTC	960
CGAGAACAGG	AGAAATCAAC	ATTGCAGTAA	CAAAAGAATG	GTTTATTATT	GCCAGTTTG	1020
GCCTCCTCAG	TGCCCTCACA	CTCTGCTACA	TGATCATCAG	AGCCACAGCT	AGCTTGAATG	1080
CTAATGAGGT	AGAATGGTTT	TGAAGAAGAA	AAAACCTGCT	TTCTGACTGA	TTTGCCCTTG	1140
AAGGAAAAAA	GAACCTATT	TTGTGCATCA	TTTACCAATC	ATGCCACACA	AGCATTATT	1200
TTTAGTACAT	TTTATTTTT	CATAAAATTG	CTAATGCCAA	AGCTTGTAT	TAAAAGAAAT	1260
AAATAATAAA	ATAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAT	TCCTGCGGCC	1320
GC						1322

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTCGGCA	CGAGGCCCTC	CCGCGCTCCC	GGGGCGCGCG	GGCCGCGCCC	CCGACGCCCT	60
ACATATACTC	AGGTGCGCCC	CACCTGTCCG	CCCGCACCTG	CTGGCTCACC	TCCGAGGCCAC	120
CTCTGCTGCG	CACCGCAGCC	TCGGACCTAC	AGCCCAGGAT	ACTTTGGGAC	TTGCCGGCGC	180
TCAGAAACGC	GCCCAGACGG	CCCCTCCACC	TTTTGTTGC	CTAGGGTCGC	CGAGAGCGCC	240
CGGAGGGAAC	CGCCTGGCCT	TCGGGGACCA	CCAATTGT	CTGGAACCAC	CCTCCCGGCG	300
TATCCTACTC	CCTGTGCCGC	GAGGCCATCG	CTTCACTGGA	GGGGTCGATT	TGTGTGTAGT	360
TTGGTGACAA	GATTGCAATT	CACCTGGCCC	AAACCCTTT	TGTCTCTTG	GGTGACCGGA	420
AAACTCCACC	TCAAGTTTC	TTTGTGGGG	CTGCCCTCCA	AGTGTGTTT	GTGTTACTGT	480
AGGGTCTCCC	GCCC GGCGCC	CCCAGTGT	TCTGAGGGCG	GAAATGGCCA	ATTGGGCCT	540
GCAGTTGCTG	GGCTTCTCCA	TGGCCCTGCT	GGGCTGGGTG	GGTCTGGTGG	CCTGCACCGC	600
CATCCCGCAG	TGGCAGATGA	GCTCCTATGC	GGGTGACAAC	ATCATCACGG	CCCAGGCCAT	660
GTACAAGGGG	CTGTGGATGG	ACTGCGTCAC	GCAGAGCACG	GGGATGATGA	GCTGAAAAT	720
GTACGACTCG	GTGCTCGCCC	TGTCCGCGGC	CTTGCAGGCC	ACTCGAGCCC	TAATGGTGGT	780
CTCCCTGGTG	CTGGGCTTCC	TGGCCATGTT	TGTGCCACG	ATGGGCATGA	AGTGCACGCG	840
CTGTGGGGAA	GACGACAAAG	TGAAGAAGGC	CCGTATAGCC	ATGGGTGGAG	GCATAATT	900
CATCGTGGCA	GGTCTGCCCC	CCTTGGTAGC	TTGCTCCTGG	TATGCCATC	AGATTGTCAC	960
AGACTTTAT	AACCCATTGA	TCCCTACCAA	CATTAAGTAT	GAGTTGGCC	CTGCCATCTT	1020
TATTGGCTGG	GCAGGGTCTG	CCCTAGTCAT	CCTGGGAGGT	GCACTGCTCT	CCTGTTCTG	1080
TCCTGGGAAT	GAGAGCAAGG	CTGGGTACCG	TGCACCCCGC	TCTTACCCCTA	AGTCCAAC	1140
TTCCAAGGAG	TATGTGTGAC	CTGGGATCTC	CTTGGCCCCAG	CCTGACAGGC	TATGGGAGTG	1200
TCTAGATGCC	TGAAAGGGCC	TGGGGCTGAG	CTCAGCCTGT	GGGCAGGGTG	CCGGACAAAG	1260
GCCTCCTGGT	CACTCTGTCC	CTGCACTCCA	TGTATAGTCC	TCTTGGGTG	GGGGTGGGG	1320
GGTGCCGTTG	GTGGGAGAGA	CAAAAAGAGG	GAGAGTGTGC	TTTTTGTACA	GTAATAAAA	1380
ATAAGTATTG	GGAAAGCAGGC	TTTTTCCCT	TCAGGGCCTC	TGCTTCCCTC	CCGTCCAGAT	1440
CCTTGAGGG	AGCTTGGAAC	CTTAGTGCAC	CTACTTCAGT	TCAGAACACT	TAGCACCCCA	1500
CTGACTCCAC	TGACAATTGA	CTAAAAGATG	CAGGTGCTCG	TATCTCGACA	TTCATTCCCCA	1560
CCCCCCCTT	ATTTAAATAG	CTACCAAAGT	ACTTCTTTT	TAATAAAA	ATAAGATT	1620

TTATTAGGTA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA	1680
AAAAAAAATT CCTGCAGGCCG C	1711

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAATTGGCA CGAGGGCAGG TCCAGAGTAA AGTCACTGAA GAGTGGAAAGC GAGGAAGGAA	60
CAGGATGATT AGACCTCAGC TGCGGACCGC GGGGCTGGGA CGATGCCTCC TGCCGGGGCT	120
GCTGCTGCTC CTGGTGCCCC TGCTCTGGGC CGGGGCTGAA AAGCTACATA CCCAGCCCTC	180
CTGCCCGCG GTCTGCCAGC CCACCGCCTG CCCCACGCGCTG CCCACCTGCG CGCTGGGGAC	240
CACGCCGGTG TTCGACCTGT GCCGCTGTTG CCGCGTCTGC CCCGCGGCCG AGCGTGAAGT	300
CTGCGGGGGG GCGCAGGGCC AACCGTGCAGC CCCGGGGCTG CAGTGCCTCC AGCCGCTGCG	360
CCCCGGGTTG CCCAGCACCT GCGGTTGCC GACGCTGGGA GGGGCCGTGT GCGGCAGCGA	420
CAGGCCACC TACCCCAGCA TGTGCGCGCT CGGGGCCGAA AACCGCGCCG CGCGCCGCCT	480
GGGCAAGGTC CCGGCCGTGC CTGTGCAGTG GGGGAACATGC GGGGATACAG GGACCAGAAAG	540
CGCAGGGCCCG CTCAGGAGGA ATTACAACCTT CATCGCCGCG GTGGTGGAGA AGGTGGCGCC	600
ATCGGTGGTT CACGTGCAGC TGTGGGGCAG GTTACTTCAC GGCAGCAGGC TTGTTCTGT	660
GTACAGTGGC TCTGGTTCA TAGTGTCTGA GGACGGGCTC ATTATTACCA ATGCCCATGT	720
TGTCAGGAAC CAGCAGTGGG TTGAGGTGGT GCTCCAGAAT GGGGCCCGTT ATGAAGCTGT	780
TGTCAAGGAT ATTGACCTTA AATTGGATCT TGCAGGTGATT AAGATTGAAT CAAATGCTGA	840
ACTTCCTGTA CTGATGCTGG GAAGATCATC TGACCTTCGG GCTGGAGAGT TTGTGGTGGC	900
TTTGGGCAGC CCATTTCTC TGCAGAACAC AGCTACTGCA GGAATTGTCA GCACCAAACA	960
GCGAGGGGGC AAAGAACTGG GGATGAAGGA TTCAGATATG GACTACGTCC AGATTGATGC	1020
CACAATTAAC TATGGGAAATT CTGGTGGTCC TCTGGTGAAC TTGGATGGTG ATGTGATTGG	1080
CGTCAATTCA TTGAGGGTGA CTGATGGAAT CTCCTTGCA ATTCCCTTCAG ATCGAGTTAG	1140
GCAGTTCTTG GCAGAATACC ATGAGCACCA GATGAAAGGA AAGGCCTTT CAAATAAGAA	1200
ATATCTGGGT CTGCAAATGC TGTCCCTCAC TGTGCCCTT AGTGAAGAAT TGAAAATGCA	1260
TTATCCAGAT TTCCCTGATG TGAGTTCTGG GGTTTATGTA TGTAAAGTGG TTGAAGGAAC	1320
AGCTGCTCAA AGCTCTGGAT TGAGAGATCA CGATGTAATT GTCAACATAA ATGGGAAACC	1380
TATTACTACT ACAACTGATG TTGTTAAAGC TCTTGACAGT GATTCCCTT CCATGGCTGT	1440
TCTTCGGGGGAA AAAGATAATT TGCTCCTGAC AGTCATACCT GAAACAATCA ATTAAATATC	1500
TTGTTTAAA GTGGGATTAT CTAAAAAAA AAAAAAAA TTCTGCAGGCC CGC	1553

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1596 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTGGCA CGAGGGGAGC CGCTCCCGGA GCCCGGCCGT AGAGGCTGCA ATCGCAGCCG	60
GGAGCCCGCA GCCCGCGCCC CGAGCCCGCC GCCGCCCTTC GAGGGCGCCC CAGGCCGCGC	120
CATGGTGAAG GTGACGTTCA ACTCCGCTCT GGCCCAGAAG GAGGCCAAGA AGGACGAGCC	180
CGAGAGCGGC GAGGAGGCC TCATCATCCC CCCCACGCC GTCGCGGTGG ACTGCAAGGA	240

CCCAGATGAT	GTGGTACCAAG	TTGGCCAAAG	AAGAGCCTGG	TGTTGGTGCA	TGTGCTTG	300
ACTAGCATT	ATGCTTGCAG	GTGTTATTCT	AGGAGGAGCA	TACTTGTACA	AATATTTGC	360
ACTTCAACCA	GATGACGTGT	ACTACTGTGG	AATAAAGTAC	ATCAAAGATG	ATGTCATCTT	420
AAATGAGCCC	TCTGCAGATG	CCCCAGCTGC	TCTCTACCAG	ACAATTGAAG	AAAATATTAA	480
AATCTTGAA	GAAGAAGAAG	TTGAATTAT	CAGTGTGCCT	GTCCCAGAGT	TTGCAGATAG	540
TGATCCTGCC	AACATTGTT	ATGACTTTAA	CAAGAAACTT	ACAGCCTATT	TAGATCTTAA	600
CCTGGATAAG	TGCTATGTGA	TCCCTCTGAA	CACTTCCATT	GTTATGCCAC	CCAGAAACCT	660
ACTGGAGTTA	CTTATTAACA	TCAAGGCTGG	AACCTATTG	CCTCAGTCCT	ATCTGATTCA	720
TGAGCACATG	GTTATTACTG	ATCGCATTGA	AAACATTGAT	CACCTGGGTT	TCTTATTTA	780
TCGACTGTGT	CATGACAAGG	AAACTTACAA	ACTGCAACGC	AGAGAAACTA	TTAAAGGTAT	840
TCAGAAACGT	GAAGCCAGCA	ATTGTTTCGC	AATTCCGCAT	TTTGAAAACA	AATTGCCGT	900
GGAAACTTA	ATTGTTCTT	GAACAGTCAA	GAAAAACATT	ATTGAGGAAA	ATTAATATCA	960
CAGCATAACC	CCACCCCTTA	CATTTGTGC	AGTGATATT	TTTAAAGTCT	CTTCATGTA	1020
AGTAGCAAAC	AGGGCTTAC	TATCTTTCA	TCTCATTAAT	TCAATTAAAA	CCATTACCTT	1080
AAAATTTTT	TCTTCGAAG	TGTGGTGTCT	TTTATATTG	AATTAGTAAC	TGTATGAAGT	1140
CATAGATAAT	AGTACATGTC	ACCTTAGGTA	GTAGGAAGAA	TTACAATTTC	TTTAAATCAT	1200
TTATCTGGAT	TTTTATGTT	TATTAGCATT	TTCAAGAAGA	CGGATTATCT	AGAGAATAAT	1260
CATATATATG	CATACGTAAA	AATGGACCAC	AGTGACTTAT	TTGTAGTTGT	TAGTTGCCCT	1320
GCTACCTAGT	TTGTTAGTGC	ATTTGAGCAC	ACATTAAAT	TTTCCTCTAA	TTAAAATGTG	1380
CAGTATTTTC	AGTGTCAAAT	ATATTTAAC	ATTTAGAGAA	TGATTCCAC	CTTTATGTTT	1440
TAATATCCTA	GGCATCTGCT	GTAATAATAT	TTTAGAAAAT	GTTTCCAATT	TAAGAAATAA	1500
CTTGTGTTAC	TAATTTGTAT	AACCCATATC	TGTGCAATGG	AATATAAATA	TCACAAAGTT	1560
GTAAAGGTTA	AAAAAAAGAA	AAATTCCCTGC	GGCCGC			1596

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met	Ala	Trp	Arg	Arg	Glu	Ala	Gly	Val	Gly	Ala	Arg	Gly	Val	Leu	
1			5			10				15					
Ala	Leu	Ala	Leu	Leu	Ala	Leu	Cys	Val	Pro	Gly	Ala	Arg	Gly		
			20			25			30						
Arg	Ala	Leu	Glu	Trp	Phe	Ser	Ala	Val	Val	Asn	Ile	Glu	Tyr	Val	Asp
			35			40				45					
Pro	Gln	Thr	Asn	Leu	Thr	Val	Trp	Ser	Val	Ser	Glu	Ser	Gly	Arg	Phe
			50			55				60					
Gly	Asp	Ser	Ser	Pro	Lys	Glu	Gly	Ala	His	Gly	Leu	Val	Gly	Val	Pro
			65			70			75			80			
Trp	Ala	Pro	Gly	Gly	Asp	Leu	Glu	Gly	Cys	Ala	Pro	Asp	Thr	Arg	Phe
			85			90			95						
Phe	Val	Pro	Glu	Pro	Gly	Gly	Arg	Gly	Ala	Ala	Pro	Trp	Val	Ala	Leu
			100			105			110						
Val	Ala	Arg	Gly	Gly	Cys	Thr	Phe	Lys	Asp	Lys	Val	Leu	Val	Ala	Ala
			115			120			125						
Arg	Arg	Asn	Ala	Ser	Ala	Val	Val	Leu	Tyr	Asn	Glu	Glu	Arg	Tyr	Gly
			130			135			140						
Asn	Ile	Thr	Leu	Pro	Met	Ser	His	Ala	Gly	Thr	Gly	Asn	Ile	Val	Val
			145			150			155			160			
Ile	Met	Ile	Ser	Tyr	Pro	Lys	Gly	Arg	Glu	Ile	Leu	Glu	Leu	Val	Gln

165	170	175
Lys Gly Ile Pro Val Thr Met Thr Ile	Gly Val Gly Thr Arg His	Val
180	185	190
Gln Glu Phe Ile Ser Gly Gln Ser Val Val Phe Val Ala Ile Ala Phe		
195	200	205
Ile Thr Met Met Ile Ile Ser Leu Ala Trp Leu Ile Phe Tyr Tyr Ile		
210	215	220
Gln Arg Phe Leu Tyr Thr Gly Ser Gln Ile Gly Ser Gln Ser His Arg		
225	230	235
Lys Glu Thr Lys Lys Val Ile Gly Gln Leu Leu Leu His Thr Val Lys		
245	250	255
His Gly Glu Lys Gly Ile Asp Val Asp Ala Glu Asn Cys Ala Val Cys		
260	265	270
Ile Glu Asn Phe Lys Val Lys Asp Ile Ile Arg Ile Leu Pro Cys Lys		
275	280	285
His Ile Phe His Arg Ile Cys Ile Asp Pro Trp Leu Leu Asp His Arg		
290	295	300
Thr Cys Pro Met Cys Lys Leu Asp Val Ile Lys Ala Leu Gly Tyr Trp		
305	310	315
Gly Glu Pro Gly Asp Val Gln Glu Met Pro Ala Pro Glu Ser Pro Pro		
325	330	335
Gly Arg Asp Pro Ala Ala Asn Leu Ser Leu Ala Leu Pro Asp Asp Asp		
340	345	350
Gly Ser Asp Asp Ser Ser Pro Pro Ser Ala Ser Pro Ala Glu Ser Glu		
355	360	365
Pro Gln Cys Asp Pro Ser Phe Lys Gly Asp Ala Gly Glu Asn Thr Ala		
370	375	380
Leu Leu Glu Ala Gly Arg Ser Asp Ser Arg His Gly Gly Pro Ile Ser		
385	390	395
		400

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Asp Lys Gly Ser Ala Gly His Pro Gly Gly Val Leu Val Trp Gly			
1	5	10	15
Arg Ser Pro Ala Pro Thr Ala Leu Trp Gly Ala Ser Pro Trp Leu Ser			
20	25	30	
Pro Leu Thr Ser Ala Leu Arg Gln Pro Leu His Arg Ala Pro Leu Leu			
35	40	45	
Pro Gly Gln Leu Cys Trp Ser Pro Arg Pro Leu Glu Lys Asn Lys Ala			
50	55	60	
Met Gly Arg Pro Leu Leu Pro Leu Leu Leu Leu Gln Pro Pro			
65	70	75	80
Ala Phe Leu Gln Pro Gly Gly Ser Thr Gly Ser Gly Pro Ser Tyr Leu			
85	90	95	
Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser			
100	105	110	
Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Ile Val			

115	120	125
Pro Asn Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser		
130	135	140
Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg		
145	150	155
Leu Phe Leu Asn Trp Thr Glu Gly Gln Glu Ser Gly Phe Leu Arg Ile		
165	170	175
Ser Asn Leu Arg Lys Glu Asp Gln Ser Val Tyr Phe Cys Arg Val Glu		
180	185	190
Leu Asp Thr Arg Arg Ser Gly Arg Gln Gln Leu Gln Ser Ile Lys Gly		
195	200	205
Thr Lys Leu Thr Ile Thr Gln Ala Val Thr Thr Thr Thr Trp Arg		
210	215	220
Pro Ser Ser Thr Thr Ile Ala Gly Leu Arg Val Thr Glu Ser Lys		
225	230	235
Gly His Ser Glu Ser Trp His Leu Ser Leu Asp Thr Ala Ile Arg Val		
245	250	255
Ala Leu Ala Val Ala Val Leu Lys Thr Val Ile Leu Gly Leu Leu Cys		
260	265	270
Leu Leu Leu Trp Trp Arg Arg Lys Gly Ser Arg Ala Pro Ser		
275	280	285
Ser Asp Phe		
290		

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Thr Val Ser Gln Arg Phe Gln Leu Ser Asn Ser Gly Pro Asn Ser		
1	5	10
15		
Thr Ile Lys Met Lys Ile Ala Leu Arg Val Leu His Leu Glu Lys Arg		
20	25	30
25		
Glu Arg Pro Pro Asp His Gln His Ser Ala Gln Val Lys Arg Pro Ser		
35	40	45
40		
Val Ser Lys Glu Gly Arg Lys Thr Ser Ile Lys Ser His Met Ser Gly		
50	55	60
55		
Ser Pro Gly Pro Gly Gly Ser Asn Thr Ala Pro Ser Thr Pro Val Ile		
65	70	75
70		
80		
Gly Gly Ser Asp Lys Pro Gly Met Glu Glu Lys Ala Gln Pro Pro Glu		
85	90	95
90		
Ala Gly Pro Gln Gly Leu His Asp Leu Gly Arg Ser Ser Ser Leu		
100	105	110
105		
Leu Ala Ser Pro Gly His Ile Ser Val Lys Glu Pro Thr Pro Ser Ile		
115	120	125
120		
Ala Ser Asp Ile Ser Leu Pro Ile Ala Thr Gln Glu Leu Arg Gln Arg		
130	135	140
135		
Leu Arg Gln Leu Glu Asn Gly Thr Thr Leu Gly Gln Ser Pro Leu Gly		
145	150	155
150		
160		
Gln Ile Gln Leu Thr Ile Arg His Ser Ser Gln Arg Asn Lys Leu Ile		

	165	170	175												
Val	Val	Val	His	Ala	Cys	Arg	Asn	Leu	Ile	Ala	Phe	Ser	Glu	Asp	Gly
	180				185								190		
Ser	Asp	Pro	Tyr	Val	Arg	Met	Tyr	Leu	Leu	Pro	Asp	Lys	Arg	Arg	Ser
	195				200							205			
Gly	Arg	Arg	Lys	Thr	His	Val	Ser	Lys	Lys	Thr	Leu	Asn	Pro	Val	Phe
	210				215						220				
Asp	Gln	Ser	Phe	Asp	Phe	Ser	Val	Ser	Leu	Pro	Glu	Val	Gln	Arg	Arg
	225				230					235			240		
Thr	Leu	Asp	Val	Ala	Val	Lys	Asn	Ser	Gly	Gly	Phe	Leu	Ser	Lys	Asp
	245				250							255			
Lys	Gly	Leu	Leu	Gly	Lys	Val	Leu	Val	Ala	Leu	Ala	Ser	Glu	Glu	Leu
	260				265							270			
Ala	Lys	Gly	Trp	Thr	Gln	Trp	Tyr	Asp	Leu	Thr	Glu	Asp	Gly	Thr	Arg
	275				280							285			
Pro	Gln	Ala	Met	Thr											
	290														

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	Glu	Arg	Arg	His	Pro	Val	Cys	Ser	Gly	Thr	Cys	Gln	Pro	Thr	Gln
						5			10				15		
Phe	Arg	Cys	Ser	Asn	Gly	Cys	Cys	Ile	Asp	Ser	Phe	Leu	Glu	Cys	Asp
						20			25				30		
Asp	Thr	Pro	Asn	Cys	Pro	Asp	Ala	Ser	Asp	Glu	Ala	Ala	Cys	Glu	Lys
						35			40				45		
Tyr	Thr	Ser	Gly	Phe	Asp	Glu	Leu	Gln	Arg	Ile	His	Phe	Pro	Ser	Asp
						50			55			60			
Lys	Gly	His	Cys	Val	Asp	Leu	Pro	Asp	Thr	Gly	Leu	Cys	Lys	Glu	Ser
						65			70			75			80
Ile	Pro	Arg	Trp	Tyr	Tyr	Asn	Pro	Phe	Ser	Glu	His	Cys	Ala	Arg	Phe
						85			90				95		
Thr	Tyr	Gly	Gly	Cys	Tyr	Gly	Asn	Lys	Asn	Asn	Phe	Glu	Glu	Gln	
						100			105			110			
Gln	Cys	Leu	Glu	Ser	Cys	Arg	Gly	Ile	Ser	Lys	Lys	Asp	Val	Phe	Gly
						115			120			125			
Leu	Arg	Arg	Glu	Ile	Pro	Ile	Pro	Ser	Thr	Gly	Ser	Val	Glu	Met	Ala
						130			135			140			
Val	Ala	Val	Phe	Leu	Val	Ile	Cys	Ile	Val	Val	Val	Val	Ala	Ile	Leu
						145			150			155			160
Gly	Tyr	Cys	Phe	Phe	Lys	Asn	Gln	Arg	Lys	Asp	Phe	His	Gly	His	His
						165			170			175			
His	His	Pro	Pro	Pro	Thr	Pro	Ala	Ser	Ser	Thr	Val	Ser	Thr	Thr	Glu
						180			185			190			
Asp	Thr	Glu	His	Leu	Val	Tyr	Asn	His	Thr	Thr	Arg	Pro	Leu		
						195			200			205			

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met	Ala	Gly	Leu	Ser	Arg	Gly	Ser	Ala	Arg	Ala	Leu	Leu	Ala	Leu	
1		5			10						15				
Leu	Ala	Ser	Thr	Leu	Leu	Ala	Leu	Leu	Val	Ser	Pro	Ala	Arg	Gly	Arg
	20				25						30				
Gly	Gly	Arg	Asp	His	Gly	Asp	Trp	Asp	Glu	Ala	Ser	Arg	Leu	Pro	Pro
	35				40						45				
Leu	Pro	Pro	Arg	Glu	Asp	Ala	Ala	Arg	Val	Ala	Arg	Phe	Val	Thr	His
	50			55					60						
Val	Ser	Asp	Trp	Gly	Ala	Leu	Ala	Thr	Ile	Ser	Thr	Leu	Glu	Ala	Val
	65			70				75			80				
Arg	Gly	Arg	Pro	Phe	Ala	Asp	Val	Leu	Ser	Leu	Ser	Asp	Gly	Pro	Pro
	85			90							95				
Gly	Ala	Gly	Ser	Gly	Val	Pro	Tyr	Phe	Tyr	Leu	Ser	Pro	Leu	Gln	Leu
	100			105						110					
Ser	Val	Ser	Asn	Leu	Gln	Glu	Asn	Pro	Tyr	Ala	Thr	Leu	Thr	Met	Thr
	115			120				125							
Leu	Ala	Gln	Thr	Asn	Phe	Cys	Lys	Lys	His	Gly	Phe	Asp	Pro	Gln	Ser
	130			135					140						
Pro	Leu	Cys	Val	His	Ile	Met	Leu	Ser	Gly	Thr	Val	Thr	Lys	Val	Asn
	145			150				155			160				
Glu	Thr	Glu	Met	Asp	Ile	Ala	Lys	His	Ser	Leu	Phe	Ile	Arg	His	Pro
	165			170					175						
Glu	Met	Lys	Thr	Trp	Pro	Ser	Ser	His	Asn	Trp	Phe	Phe	Ala	Lys	Leu
	180			185				190							
Asn	Ile	Thr	Asn	Ile	Trp	Val	Leu	Asp	Tyr	Phe	Gly	Gly	Pro	Lys	Ile
	195			200				205							
Val	Thr	Pro	Glu	Glu	Tyr	Tyr	Asn	Val	Thr	Val	Gln				
	210			215				220							

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met	Asp	His	His	Cys	Pro	Trp	Leu	Asn	Asn	Cys	Val	Gly	His	Tyr	Asn
1		5			10						15				
His	Arg	Tyr	Phe	Phe	Ser	Phe	Cys	Phe	Phe	Met	Thr	Leu	Gly	Cys	Val
	20			25						30					

Tyr Cys Ser Tyr Gly Ser Trp Asp Leu Phe Arg Glu Ala Tyr Ala Ala
 35 40 45
 Ile Glu Lys Met Lys Gln Leu Asp Lys Asn Lys Leu Gln Ala Val Ala
 50 55 60
 Asn Gln Thr Tyr His Gln Thr Pro Pro Pro Thr Phe Ser Phe Arg Glu
 65 70 75 80
 Arg Met Thr His Lys Ser Leu Val Tyr Leu Trp Phe Leu Cys Ser Ser
 85 90 95
 Val Ala Leu Ala Leu Gly Ala Leu Thr Val Trp His Ala Val Leu Ile
 100 105 110
 Ser Arg Gly Glu Thr Ser Ile Glu Arg His Ile Asn Lys Lys Glu Arg
 115 120 125
 Arg Arg Leu Gln Ala Lys Gly Arg Val Phe Arg Asn Pro Tyr Asn Tyr
 130 135 140
 Gly Cys Leu Asp Asn Trp Lys Val Phe Leu Gly Val Asp Thr Gly Arg
 145 150 155 160
 His Trp Leu Thr Arg Val Leu Leu Pro Ser Thr His Leu Pro His Gly
 165 170 175
 Asn Gly Met Ser Trp Glu Pro Pro Trp Val Thr Ala His Ser Ala
 180 185 190
 Ser Val Met Ala Val
 195

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Ala Pro Leu Gly Met Leu Leu Gly Leu Leu Met Ala Ala Cys Phe
 1 5 10 15
 Thr Phe Cys Leu Ser His Gln Asn Leu Lys Glu Phe Ala Leu Thr Asn
 20 25 30
 Pro Glu Lys Ser Ser Thr Lys Glu Thr Glu Arg Lys Glu Thr Lys Ala
 35 40 45
 Glu Glu Glu Leu Asp Ala Glu Val Leu Glu Val Phe His Pro Thr His
 50 55 60
 Glu Trp Gln Ala Leu Gln Pro Gly Gln Ala Val Pro Ala Gly Ser His
 65 70 75 80
 Val Arg Leu Asn Leu Gln Thr Gly Glu Arg Glu Ala Lys Leu Gln Tyr
 85 90 95
 Glu Asp Lys Phe Arg Asn Asn Leu Lys Gly Lys Arg Leu Asp Ile Asn
 100 105 110
 Thr Asn Thr Tyr Thr Ser Gln Asp Leu Lys Ser Ala Leu Ala Lys Phe
 115 120 125
 Lys Glu Gly Ala Glu Met Glu Ser Ser Lys Glu Asp Lys Ala Arg Gln
 130 135 140
 Ala Glu Val Lys Arg Leu Phe Arg Pro Ile Glu Glu Leu Lys Lys Asp
 145 150 155 160
 Phe Asp Glu Leu Asn Val Val Ile Glu Thr Asp Met Gln Ile Met Val
 165 170 175

Arg Leu Ile Asn Lys Phe Asn Ser Ser Ser Ser Ser Leu Glu Glu Lys
 180 185 190
 Ile Ala Ala Leu Phe Asp Leu Glu Tyr Tyr Val His Gln Met Asp Asn
 195 200 205
 Ala Gln Asp Leu Leu Ser Phe Gly Gly Leu Gln Val Val Ile Asn Gly
 210 215 220
 Leu Asn Ser Thr Glu Pro Leu Val Lys Glu Tyr Ala Ala Phe Val Leu
 225 230 235 240
 Gly Ala Ala Phe Ser Ser Asn Pro Lys Val Gln Val Glu Ala Ile Glu
 245 250 255
 Gly Gly Ala Leu Gln Lys Leu Leu Val Ile Leu Ala Thr Glu Gln Pro
 260 265 270
 Leu Thr Ala Lys Lys Val Leu Phe Ala Leu Cys Ser Leu Leu Arg
 275 280 285
 His Phe Pro Tyr Ala Gln Arg Gln Phe Leu Lys Leu Gly Gly Leu Gln
 290 295 300
 Val Leu Arg Thr Leu Val Gln Glu Lys Gly Thr Glu Val Leu Ala Val
 305 310 315 320
 Arg Val Val Thr Leu Leu Tyr Asp Leu Val Thr Glu Lys Met Phe Ala
 325 330 335
 Glu Glu Glu Ala Glu Leu Thr Gln Glu Met Ser Pro Glu Lys Leu Gln
 340 345 350
 Gln Tyr Arg Gln Val His Leu Leu Pro Gly Leu Trp Glu Gln Gly Trp
 355 360 365
 Cys Glu Ile Thr Ala His Leu Leu Ala Leu Pro Glu His Asp Ala Arg
 370 375 380
 Glu Lys Val Leu Gln Thr Leu Gly Val Leu Leu Thr Thr Cys Arg Asp
 385 390 395 400
 Arg Tyr Arg Gln Asp Pro Gln Leu Gly Arg Thr Leu Ala Ser Leu Gln
 405 410 415
 Ala Glu Tyr Gln Val Leu Ala Ser Leu Glu Leu Gln Asp Gly Glu Asp
 420 425 430
 Glu Gly Tyr Phe Gln Glu Leu Leu Gly Ser Val Asn Ser Leu Leu Lys
 435 440 445
 Glu Leu Arg
 450

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Trp Gln Ala Gly Lys Arg Gln Ala Ser Arg Ala Phe Ser Leu Tyr
 1 5 10 15
 Ala Asn Ile Asp Ile Leu Arg Pro Tyr Phe Asp Val Glu Pro Ala Gln
 20 25 30
 Val Arg Ser Arg Leu Leu Glu Ser Met Ile Pro Ile Lys Met Val Asn
 35 40 45
 Phe Pro Gln Lys Ile Ala Gly Glu Leu Tyr Gly Pro Leu Met Leu Val
 50 55 60

Phe Thr Leu Val Ala Ile Leu Leu His Gly Met Lys Thr Ser Asp Thr
 65 70 75 80
 Ile Ile Arg Glu Gly Thr Leu Met Gly Thr Ala Ile Gly Thr Cys Phe
 85 90 95
 Gly Tyr Trp Leu Gly Val Ser Ser Phe Ile Tyr Phe Leu Ala Tyr Leu
 100 105 110
 Cys Asn Ala Gln Ile Thr Met Leu Gln Met Leu Ala Leu Leu Gly Tyr
 115 120 125
 Gly Leu Phe Gly His Cys Ile Val Leu Phe Ile Thr Tyr Asn Ile His
 130 135 140
 Leu His Ala Leu Phe Tyr Leu Phe Trp Leu Leu Val Gly Gly Leu Ser
 145 150 155 160
 Thr Leu Arg Met Val Ala Val Leu Val Ser Arg Thr Val Gly Pro Thr
 165 170 175
 Gln Arg Leu Leu Leu Cys Gly Thr Leu Ala Ala Leu His Met Leu Phe
 180 185 190
 Leu Leu Tyr Leu His Phe Ala Tyr His Lys Val Val Glu Gly Ile Leu
 195 200 205
 Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro Ile Gln Arg Val Pro Arg
 210 215 220
 Asp Ile Pro Ala Met Leu Pro Ala Ala Arg Leu Pro Thr Thr Val Leu
 225 230 235 240
 Asn Ala Thr Ala Lys Ala Val Ala Val Thr Leu Gln Ser His
 245 250

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Gly Ser Glu Asn Glu Ala Leu Asp Leu Ser Met Lys Ser Val Pro
 1 5 10 15
 Trp Leu Lys Ala Gly Glu Val Ser Pro Pro Ile Phe Gln Glu Asp Ala
 20 25 30
 Ala Leu Asp Leu Ser Val Ala Ala His Arg Lys Ser Glu Pro Pro Pro
 35 40 45
 Glu Thr Leu Tyr Asp Ser Gly Ala Ser Val Asp Ser Ser Gly His Thr
 50 55 60
 Val Met Glu Lys Leu Pro Ser Gly Met Glu Ile Ser Phe Ala Pro Ala
 65 70 75 80
 Thr Ser His Glu Ala Pro Ala Met Met Asp Ser His Ile Ser Ser Ser
 85 90 95
 Asp Ala Ala Thr Glu Met Leu Ser Gln Pro Asn His Pro Ser Gly Glu
 100 105 110
 Val Lys Ala Glu Asn Asn Ile Glu Met Val Gly Glu Ser Gln Ala Ala
 115 120 125
 Lys Val Ile Val Ser Val Glu Asp Ala Val Pro Thr Ile Phe Cys Gly
 130 135 140
 Lys Ile Lys Gly Leu Ser Gly Val Ser Thr Lys Asn Phe Ser Phe Lys
 145 150 155 160

Arg	Glu	Asp	Ser	Val	Leu	Gln	Gly	Tyr	Asp	Ile	Asn	Ser	Gln	Gly	Glu
165															175
Glu	Ser	Met	Gly	Asn	Ala	Glu	Pro	Leu	Arg	Lys	Pro	Ile	Lys	Asn	Arg
180															190
Ser	Ile	Lys	Leu	Lys	Lys	Val	Asn	Ser	Gln	Glu	Val	His	Met	Leu	Pro
195															205
Ile	Lys	Lys	Gln	Arg	Leu	Ala	Thr	Phe	Phe	Pro	Arg	Lys			
210															220

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met	Val	Lys	Val	Thr	Phe	Asn	Ser	Ala	Leu	Ala	Gln	Lys	Glu	Ala	Lys
1															15
Lys	Asp	Glu	Pro	Lys	Ser	Gly	Glu	Glu	Ala	Leu	Ile	Ile	Pro	Pro	Asp
															30
20															
Ala	Val	Ala	Val	Asp	Cys	Lys	Asp	Pro	Asp	Asp	Val	Val	Pro	Val	Gly
35															45
Gln	Arg	Arg	Ala	Trp	Cys	Trp	Cys	Met	Cys	Phe	Gly	Leu	Ala	Phe	Met
50															60
Leu	Ala	Gly	Val	Ile	Leu	Gly	Gly	Ala	Tyr	Leu	Tyr	Lys	Tyr	Phe	Ala
65															80
Leu	Gln	Pro	Asp	Asp	Val	Tyr	Tyr	Cys	Gly	Ile	Lys	Tyr	Ile	Lys	Asp
85															95
Asp	Val	Ile	Leu	Asn	Glu	Pro	Ser	Ala	Asp	Ala	Pro	Ala	Ala	Leu	Tyr
100															110
Gln	Thr	Ile	Glu	Glu	Asn	Ile	Lys	Ile	Phe	Glu	Glu	Glu	Val	Glu	
115															125
Phe	Ile	Ser	Val	Pro	Val	Pro	Glu	Phe	Ala	Asp	Ser	Asp	Pro	Ala	Asn
130															140
Ile	Val	His	Asp	Phe	Asn	Lys	Lys	Leu	Thr	Ala	Tyr	Leu	Asp	Leu	Asn
145															160
Leu	Asp	Lys	Cys	Tyr	Val	Ile	Pro	Leu	Asn	Thr	Ser	Ile	Val	Met	Pro
165															175
Pro	Arg	Asn	Leu	Leu	Glu	Leu	Ile	Asn	Ile	Lys	Ala	Gly	Thr	Tyr	
180															190
Leu	Pro	Gln	Ser	Tyr	Leu	Ile	His	Glu	His	Met	Val	Ile	Thr	Asp	Arg
195															205
Ile	Glu	Asn	Ile	Asp	His	Leu	Gly	Phe	Phe	Ile	Tyr	Arg	Leu	Cys	His
210															220
Asp	Lys	Glu	Thr	Tyr	Lys	Leu	Gln	Arg	Arg	Glu	Thr	Ile	Lys	Gly	Ile
225															240
Gln	Lys	Arg	Glu	Ala	Ser	Asn	Cys	Phe	Ala	Ile	Arg	His	Phe	Glu	Asn
245															255
Lys	Phe	Ala	Val	Glu	Thr	Leu	Ile	Cys	Ser						
260															

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met	Pro	Thr	Gly	Asp	Phe	Asp	Ser	Lys	Pro	Ser	Trp	Ala	Asp	Gln	Val
1			5					10						15	
Glu	Glu	Glu	Gly	Glu	Asp	Asp	Lys	Cys	Val	Thr	Ser	Glu	Leu	Leu	Lys
			20					25						30	
Gly	Ile	Pro	Leu	Ala	Thr	Gly	Asp	Thr	Ser	Pro	Glu	Pro	Glu	Leu	Leu
			35				40						45		
Pro	Gly	Ala	Pro	Leu	Pro	Pro	Pro	Lys	Glu	Val	Ile	Asn	Gly	Asn	Ile
			50				55					60			
Lys	Thr	Val	Thr	Glu	Tyr	Lys	Ile	Asp	Glu	Asp	Gly	Lys	Lys	Phe	Lys
			65				70				75			80	
Ile	Val	Arg	Thr	Phe	Arg	Ile	Glu	Thr	Arg	Lys	Ala	Ser	Lys	Ala	Val
						85			90				95		
Ala	Arg	Arg	Lys	Asn	Trp	Lys	Lys	Phe	Gly	Asn	Ser	Glu	Phe	Asp	Pro
			100				105					110			
Pro	Gly	Pro	Asn	Val	Ala	Thr	Thr	Thr	Val	Ser	Asp	Asp	Val	Ser	Met
						115		120				125			
Thr	Phe	Ile	Thr	Ser	Lys	Glu	Asp	Leu	Asn	Cys	Gln	Glu	Glu	Asp	
			130			135					140				
Pro	Met	Asn	Lys	Phe	Lys	Gly	Gln	Lys	Ile	Val	Ser	Cys	Arg	Ile	Cys
			145			150				155			160		
Lys	Gly	Asp	His	Trp	Thr	Thr	Arg	Cys	Pro	Tyr	Lys	Asp	Thr	Leu	Gly
						165				170			175		
Pro	Met	Gln	Lys	Glu	Leu	Ala	Glu	Gln	Leu	Gly	Leu	Ser	Thr	Gly	Glu
						180		185				190			
Lys	Glu	Lys	Leu	Pro	Gly	Glu	Leu	Glu	Pro	Val	Gln	Ala	Thr	Gln	Asn
			195			200					205				
Lys	Thr	Gly	Lys	Tyr	Val	Pro	Pro	Ser	Leu	Arg	Asp	Gly	Ala	Ser	Arg
			210			215					220				
Arg	Gly	Glu	Ser	Met	Gln	Pro	Asn	Arg	Arg	Ala	Asp	Asp	Asn	Ala	Thr
			225			230					235			240	
Ile	Arg	Val	Thr	Asn	Leu	Arg	Arg	Gly	His	Ala					
					245			250							

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met Arg Arg Leu Asn Arg Lys Lys Thr Leu Ser Leu Val Lys Glu Leu

1	5	10	15												
Asp	Ala	Phe	Pro	Lys	Val	Pro	Glu	Ser	Tyr	Val	Glu	Thr	Ser	Ala	Ser
				20				25							30
Gly	Gly	Thr	Val	Ser	Leu	Ile	Ala	Phe	Thr	Thr	Met	Ala	Leu	Leu	Thr
				35				40							45
Ile	Met	Glu	Phe	Ser	Val	Tyr	Gln	Asp	Thr	Trp	Met	Lys	Tyr	Glu	Tyr
				50				55							60
Glu	Val	Asp	Lys	Asp	Phe	Ser	Ser	Lys	Leu	Arg	Ile	Asn	Ile	Asp	Ile
				65				70							80
Thr	Val	Ala	Met	Lys	Cys	Gln	Tyr	Val	Gly	Ala	Asp	Val	Leu	Asp	Leu
				85				90							95
Ala	Glu	Thr	Met	Val	Ala	Ser	Ala	Asp	Gly	Leu	Val	Tyr	Glu	Pro	Thr
				100				105							110
Val	Phe	Asp	Leu	Ser	Pro	Gln	Gln	Lys	Glu	Trp	Gln	Arg	Met	Leu	Gln
				115				120							125
Leu	Ile	Gln	Ser	Arg	Leu	Gln	Glu	Glu	His	Ser	Leu	Gln	Asp	Val	Ile
				130				135							140
Phe	Lys	Ser	Ala	Phe	Lys	Ser	Thr	Ser	Thr	Ala	Leu	Pro	Pro	Arg	Glu
				145				150							160
Asp	Asp	Ser	Ser	Gln	Ser	Pro	Asn	Ala	Cys	Arg	Ile	His	Gly	His	Leu
				165				170							175
Tyr	Val	Asn	Lys	Val	Ala	Gly	Asn	Phe	His	Ile	Thr	Val	Gly	Lys	Ala
				180				185							190
Ile	Pro	His	Pro	Arg	Gly	His	Ala	His	Leu	Ala	Ala	Leu	Val	Asn	His
				195				200							205
Glu	Ser	Tyr	Asn	Phe	Ser	His	Arg	Ile	Asp	His	Leu	Ser	Phe	Gly	Glu
				210				215							220
Leu	Val	Pro	Ala	Ile	Ile	Asn	Pro	Leu	Asp	Gly	Thr	Glu	Lys	Ile	Ala
				225				230							240
Ile	Asp	His	Asn	Gln	Met	Phe	Gln	Tyr	Phe	Ile	Thr	Val	Val	Pro	Thr
				245				250							255
Lys	Leu	His	Thr	Tyr	Lys	Ile	Ser	Ala	Asp	Thr	His	Gln	Phe	Ser	Val
				260				265							270
Thr	Glu	Arg	Glu	Arg	Ile	Ile	Asn	His	Ala	Ala	Gly	Ser	His	Gly	Val
				275				280							285
Ser	Gly	Ile	Phe	Met	Lys	Tyr	Asp	Leu	Ser	Ser	Leu	Met	Val	Thr	Val
				290				295							300
Thr	Glu	Glu	His	Met	Pro	Phe	Trp	Gln	Phe	Phe	Val	Arg	Leu	Cys	Gly
				305				310							320
Ile	Val	Gly	Gly	Ile	Phe	Ser	Thr	Thr	Gly	Met	Leu	His	Gly	Ile	Gly
				325				330							335
Lys	Phe	Ile	Val	Glu	Ile	Ile	Cys	Cys	Arg	Phe	Arg	Leu	Gly	Ser	Tyr
				340				345							350
Lys	Pro	Val	Asn	Ser	Val	Pro	Phe	Glu	Asp	Gly	His	Thr	Asp	Asn	His
				355				360							365
Leu	Pro	Leu	Leu	Glu	Asn	Asn	Thr	His							
								375							

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met	Gly	Ser	Gln	His	Ser	Ala	Ala	Ala	Arg	Pro	Ser	Ser	Cys	Arg	Arg
1															15
Lys	Gln	Glu	Asp	Asp	Arg	Asp	Gly	Leu	Leu	Ala	Glu	Arg	Glu	Gln	Glu
								20		25					30
Glu	Ala	Ile	Ala	Gln	Phe	Pro	Tyr	Val	Glu	Phe	Thr	Gly	Arg	Asp	Ser
								35		40					45
Ile	Thr	Cys	Leu	Thr	Cys	Gln	Gly	Thr	Gly	Tyr	Ile	Pro	Thr	Glu	Gln
								50		55					60
Val	Asn	Glu	Leu	Val	Ala	Leu	Ile	Pro	His	Ser	Asp	Gln	Arg	Leu	Arg
65								70		75					80
Pro	Gln	Arg	Thr	Lys	Gln	Tyr	Val	Leu	Leu	Ser	Ile	Leu	Leu	Cys	Leu
								85		90					95
Leu	Ala	Ser	Gly	Leu	Val	Val	Phe	Phe	Leu	Phe	Pro	His	Ser	Val	Leu
								100		105					110
Val	Asp	Asp	Asp	Gly	Ile	Lys	Val	Val	Lys	Val	Thr	Phe	Asn	Lys	Gln
								115		120					125
Asp	Ser	Leu	Val	Ile	Leu	Thr	Ile	Met	Ala	Thr	Leu	Lys	Ile	Arg	Asn
								130		135					140
Ser	Asn	Phe	Tyr	Thr	Val	Ala	Val	Thr	Ser	Leu	Ser	Ser	Gln	Ile	Gln
145								150		155					160
Tyr	Met	Asn	Thr	Val	Val	Ser	Thr	Tyr	Val	Thr	Thr	Asn	Val	Ser	Leu
								165		170					175
Ile	Pro	Pro	Arg	Ser	Glu	Gln	Leu	Val	Asn	Phe	Thr	Gly	Lys	Ala	Glu
								180		185					190
Met	Gly	Gly	Pro	Phe	Ser	Tyr	Val	Tyr	Phe	Phe	Cys	Thr	Val	Pro	Glu
								195		200					205
Ile	Leu	Val	His	Asn	Ile	Val	Ile	Phe	Met	Arg	Thr	Ser	Val	Lys	Ile
								210		215					220
Ser	Tyr	Ile	Gly	Leu	Met	Thr	Gln	Ser	Ser	Leu	Glu	Thr	His	His	Tyr
225								225		230					240
Val	Asp	Cys	Gly	Gly	Asn	Ser	Thr	Ala	Ile						
								245		250					

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met	Val	Thr	Cys	Phe	His	Val	Pro	Tyr	Ser	Ala	Leu	Thr	Met	Phe	Ile
1															15
Ser	Thr	Glu	Gln	Thr	Glu	Arg	Asp	Ser	Ala	Thr	Ala	Tyr	Arg	Met	Thr
								20		25					30
Val	Glu	Val	Leu	Gly	Thr	Val	Leu	Gly	Thr	Ala	Ile	Gln	Gly	Gln	Ile
								35		40					45
Val	Gly	Gln	Ala	Asp	Thr	Pro	Cys	Phe	Gln	Asp	Leu	Asn	Ser	Ser	Thr
								50		55					60
Val	Ala	Ser	Gln	Ser	Ala	Asn	His	Thr	His	Gly	Thr	Thr	Ser	His	Arg

65	70	75	80												
Glu	Thr	Gln	Lys	Ala	Tyr	Leu	Leu	Ala	Ala	Gly	Val	Ile	Val	Cys	Ile
			85			90							95		
Tyr	Ile	Ile	Cys	Ala	Val	Ile	Leu	Ile	Leu	Gly	Val	Arg	Glu	Gln	Arg
			100			105						110			
Glu	Pro	Tyr	Glu	Ala	Gln	Gln	Ser	Glu	Pro	Ile	Ala	Tyr	Phe	Arg	Gly
			115			120						125			
Leu	Arg	Leu	Val	Met	Ser	His	Gly	Pro	Tyr	Ile	Lys	Leu	Ile	Thr	Gly
			130			135					140				
Phe	Leu	Phe	Thr	Ser	Leu	Ala	Phe	Met	Leu	Val	Glu	Gly	Asn	Phe	Val
			145			150				155			160		
Leu	Phe	Cys	Thr	Tyr	Thr	Leu	Gly	Phe	Arg	Asn	Glu	Phe	Gln	Asn	Leu
			165			170						175			
Leu	Leu	Ala	Ile	Met	Leu	Ser	Ala	Thr	Leu	Thr	Ile	Pro	Ile	Trp	Gln
			180			185					190				
Trp	Phe	Leu	Thr	Arg	Phe	Gly	Lys	Lys	Thr	Ala	Val	Tyr	Val	Gly	Ile
			195			200					205				
Ser	Ser	Ala	Val	Pro	Phe	Leu	Ile	Leu	Val	Ala	Leu	Met	Glu	Ser	Asn
			210			215					220				
Leu	Ile	Ile	Thr	Tyr	Ala	Val	Ala	Val	Ala	Gly	Ile	Ser	Val	Ala	
			225			230				235			240		
Ala	Ala	Phe	Leu	Leu	Pro	Trp	Ser	Met	Leu	Pro	Asp	Val	Ile	Asp	Asp
			245			250					255				
Phe	His	Leu	Lys	Gln	Pro	His	Phe	His	Gly	Thr	Glu	Pro	Ile	Phe	Phe
			260			265					270				
Ser	Phe	Tyr	Val	Phe	Phe	Thr	Lys	Phe	Ala	Ser	Gly	Val	Ser	Leu	Gly
			275			280					285				
Ile	Ser	Thr	Leu	Ser	Leu	Asp	Phe	Ala	Gly	Tyr	Gln	Thr	Arg	Gly	Cys
			290			295					300				
Ser	Gln	Pro	Glu	Arg	Val	Lys	Phe	Thr	Leu	Asn	Met	Leu	Val	Thr	Met
			305			310				315			320		
Ala	Pro	Ile	Val	Leu	Ile	Leu	Leu	Gly	Leu	Leu	Phe	Lys	Met	Tyr	
			325			330					335				
Pro	Ile	Asp	Glu	Glu	Arg	Arg	Arg	Gln	Asn	Lys	Lys	Ala	Leu	Gln	Ala
			340			345					350				
Leu	Arg	Asp	Glu	Ala	Ser	Ser	Ser	Gly	Cys	Ser	Glu	Thr	Asp	Ser	Thr
			355			360					365				
Glu	Leu	Ala	Ser	Ile	Leu										
			370												

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met	Val	Asn	Asp	Pro	Pro	Val	Pro	Ala	Leu	Leu	Trp	Ala	Gln	Glu	Val
1				5					10				15		
Gly	Gln	Val	Leu	Ala	Gly	Arg	Ala	Arg	Arg	Leu	Leu	Leu	Gln	Phe	Gly
						20			25				30		
Val	Leu	Phe	Cys	Thr	Ile	Leu	Leu	Leu	Leu	Trp	Val	Ser	Val	Phe	Leu

35	40	45													
Tyr	Gly	Ser	Phe	Tyr	Tyr	Ser	Tyr	Met	Pro	Thr	Val	Ser	His	Leu	Ser
50															
55															60
Pro	Val	His	Phe	Tyr	Tyr	Arg	Thr	Asp	Cys	Asp	Ser	Ser	Thr	Thr	Ser
65															80
70															75
Leu	Cys	Ser	Phe	Pro	Val	Ala	Asn	Val	Ser	Leu	Thr	Lys	Gly	Gly	Arg
															85
															90
85															95
Asp	Arg	Val	Leu	Met	Tyr	Gly	Gln	Pro	Tyr	Arg	Val	Thr	Leu	Glu	Leu
															100
															105
100															110
Glu	Leu	Pro	Glu	Ser	Pro	Val	Asn	Gln	Asp	Leu	Gly	Met	Phe	Leu	Val
															115
															120
115															125
Thr	Ile	Ser	Cys	Tyr	Thr	Arg	Gly	Gly	Arg	Ile	Ile	Ser	Thr	Ser	Ser
															130
															135
130															140
Arg	Ser	Val	Met	Leu	His	Tyr	Arg	Ser	Asp	Leu	Leu	Gln	Met	Leu	Asp
															145
															150
145															155
Thr	Leu	Val	Phe	Ser	Ser	Leu	Leu	Leu	Phe	Gly	Phe	Ala	Glu	Gln	Lys
															165
															170
165															175
Gln	Leu	Leu	Glu	Val	Glu	Leu	Tyr	Ala	Asp	Tyr	Arg	Glu	Asn	Ser	Tyr
															180
															185
180															190
Val	Pro	Thr	Thr	Gly	Ala	Ile	Ile	Glu	Ile	His	Ser	Lys	Arg	Ile	Gln
															195
															200
195															205
Leu	Tyr	Gly	Ala	Tyr	Leu	Arg	Ile	His	Ala	His	Phe	Thr	Gly	Leu	Arg
															210
															215
210															220
Tyr	Leu	Leu	Tyr	Asn	Phe	Pro	Met	Thr	Cys	Ala	Phe	Ile	Gly	Val	Ala
															225
															230
225															235
Ser	Asn	Phe	Thr	Phe	Leu	Ser	Val	Ile	Val	Leu	Phe	Ser	Tyr	Met	Gln
															245
															250
245															255
Trp	Val	Trp	Gly	Gly	Ile	Trp	Pro	Arg	His	Arg	Phe	Ser	Leu	Gln	Val
															260
															265
260															270
Asn	Ile	Arg	Lys	Arg	Asp	Asn	Ser	Arg	Lys	Glu	Val	Gln	Arg	Arg	Ile
															275
															280
275															285
Ser	Ala	His	Gln	Pro	Gly	Pro	Glu	Gly	Gln	Glu	Glu	Ser	Thr	Pro	Gln
															290
															295
290															300
Ser	Asp	Val	Thr	Glu	Asp	Gly	Glu	Ser	Pro	Glu	Asp	Pro	Ser	Gly	Thr
															305
															310
305															315
Glu	Val	Ser	Cys	Pro	Arg	Arg	Arg	Asn	Gln	Ile	Ser	Ser	Pro		
															325
															330

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met	Thr	His	Pro	Gly	Thr	Gly	Asp	Ile	Ile	Ala	Val	Met	Ile	Thr	Glu
1															15
Leu	Arg	Gly	Lys	Asp	Ile	Leu	Ser	Tyr	Leu	Glu	Lys	Asn	Ile	Ser	Val
															20
															25
															30
Gln	Met	Thr	Ile	Ala	Val	Gly	Thr	Arg	Met	Pro	Pro	Lys	Asn	Phe	Ser
															35
															40
															45
Arg	Gly	Ser	Leu	Val	Phe	Val	Ser	Ile	Ser	Phe	Ile	Val	Leu	Met	Ile

50	55	60
Ile Ser Ser Ala Trp Leu Ile Phe Tyr Phe Ile Gln Lys Ile Arg Tyr		
65	70	75
Thr Asn Ala Arg Asp Arg Asn Gln Arg Arg Leu Gly Asp Ala Ala Lys		
	85	90
Lys Ala Ile Ser Lys Leu Thr Thr Arg Thr Val Lys Lys Gly Asp Lys		
	100	105
Glu Thr Asp Pro Asp Phe Asp His Cys Ala Val Cys Ile Glu Ser Tyr		
	115	120
Cys Lys Asn Asp Val Val Arg Ile Leu Pro Cys Lys His Val Phe His		
	130	135
Lys Ser Cys Val Asp Pro Trp Leu Ser Glu His Cys Thr Cys Pro Met		
	145	150
Cys Lys Leu Asn Ile Leu Lys Ala Leu Gly Ile Val Pro Asn Leu Pro		
	165	170
Cys Thr Asp Asn Val Ala Phe Asp Met Glu Arg Leu Thr Arg Thr Gln		
	180	185
Ala Val Asn Arg Arg Ser Ala Leu Gly Asp Leu Ala Gly Asp Asn Ser		
	195	200
Leu Gly Leu Glu Pro Leu Arg Thr Ser Gly Ile Ser Pro Leu Pro Gln		
	210	215
Asp Gly Glu Leu Thr Pro Arg Thr Gly Glu Ile Asn Ile Ala Val Thr		
	225	230
Lys Glu Trp Phe Ile Ile Ala Ser Phe Gly Leu Leu Ser Ala Leu Thr		
	245	250
Leu Cys Tyr Met Ile Ile Arg Ala Thr Ala Ser Leu Asn Ala Asn Glu		
	260	265
Val Glu Trp Phe		
	275	

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Ala Asn Ser Gly Leu Gln Leu Leu Gly Phe Ser Met Ala Leu Leu		
1	5	10
Gly Trp Val Gly Leu Val Ala Cys Thr Ala Ile Pro Gln Trp Gln Met		
	20	25
Ser Ser Tyr Ala Gly Asp Asn Ile Ile Thr Ala Gln Ala Met Tyr Lys		
	35	40
Gly Leu Trp Met Asp Cys Val Thr Gln Ser Thr Gly Met Met Ser Cys		
	50	55
Lys Met Tyr Asp Ser Val Leu Ala Leu Ser Ala Ala Leu Gln Ala Thr		
	65	70
Arg Ala Leu Met Val Val Ser Leu Val Leu Gly Phe Leu Ala Met Phe		
	85	90
Val Ala Thr Met Gly Met Lys Cys Thr Arg Cys Gly Gly Asp Asp Lys		
	100	105
Val Lys Lys Ala Arg Ile Ala Met Gly Gly Gly Ile Ile Phe Ile Val		

115	120	125
Ala Gly Leu Ala Ala Leu Val Ala Cys Ser Trp Tyr Gly His Gln Ile		
130	135	140
Val Thr Asp Phe Tyr Asn Pro Leu Ile Pro Thr Asn Ile Lys Tyr Glu		
145	150	155
Phe Gly Pro Ala Ile Phe Ile Gly Trp Ala Gly Ser Ala Leu Val Ile		
165	170	175
Leu Gly Gly Ala Leu Leu Ser Cys Ser Cys Pro Gly Asn Glu Ser Lys		
180	185	190
Ala Gly Tyr Arg Ala Pro Arg Ser Tyr Pro Lys Ser Asn Ser Ser Lys		
195	200	205
Glu Tyr		
210		

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Ile Arg Pro Gln Leu Arg Thr Ala Gly Leu Gly Arg Cys Leu Leu		
1	5	10
		15
Pro Gly Leu Leu Leu Leu Val Pro Val Leu Trp Ala Gly Ala Glu		
20	25	30
Lys Leu His Thr Gln Pro Ser Cys Pro Ala Val Cys Gln Pro Thr Arg		
35	40	45
Cys Pro Ala Leu Pro Thr Cys Ala Leu Gly Thr Thr Pro Val Phe Asp		
50	55	60
Leu Cys Arg Cys Cys Arg Val Cys Pro Ala Ala Glu Arg Glu Val Cys		
65	70	75
		80
Gly Gly Ala Gln Gly Gln Pro Cys Ala Pro Gly Leu Gln Cys Leu Gln		
85	90	95
Pro Leu Arg Pro Gly Phe Pro Ser Thr Cys Gly Cys Pro Thr Leu Gly		
100	105	110
Gly Ala Val Cys Gly Ser Asp Arg Arg Thr Tyr Pro Ser Met Cys Ala		
115	120	125
Leu Arg Ala Glu Asn Arg Ala Ala Arg Arg Leu Gly Lys Val Pro Ala		
130	135	140
Val Pro Val Gln Trp Gly Asn Cys Gly Asp Thr Gly Thr Arg Ser Ala		
145	150	155
		160
Gly Pro Leu Arg Arg Asn Tyr Asn Phe Ile Ala Ala Val Val Glu Lys		
165	170	175
Val Ala Pro Ser Val Val His Val Gln Leu Trp Gly Arg Leu Leu His		
180	185	190
Gly Ser Arg Leu Val Pro Val Tyr Ser Gly Ser Gly Phe Ile Val Ser		
195	200	205
Glu Asp Gly Leu Ile Ile Thr Asn Ala His Val Val Arg Asn Gln Gln		
210	215	220
Trp Ile Glu Val Val Leu Gln Asn Gly Ala Arg Tyr Glu Ala Val Val		
225	230	235
		240
Lys Asp Ile Asp Leu Lys Leu Asp Leu Ala Val Ile Lys Ile Glu Ser		

245	250	255
Asn Ala Glu Leu Pro Val Leu Met Leu Gly Arg Ser Ser Asp Leu Arg		
260	265	270
Ala Gly Glu Phe Val Val Ala Leu Gly Ser Pro Phe Ser Leu Gln Asn		
275	280	285
Thr Ala Thr Ala Gly Ile Val Ser Thr Lys Gln Arg Gly Gly Lys Glu		
290	295	300
Leu Gly Met Lys Asp Ser Asp Met Asp Tyr Val Gln Ile Asp Ala Thr		
305	310	315
Ile Asn Tyr Gly Asn Ser Gly Gly Pro Leu Val Asn Leu Asp Gly Asp		
325	330	335
Val Ile Gly Val Asn Ser Leu Arg Val Thr Asp Gly Ile Ser Phe Ala		
340	345	350
Ile Pro Ser Asp Arg Val Arg Gln Phe Leu Ala Glu Tyr His Glu His		
355	360	365
Gln Met Lys Gly Lys Ala Phe Ser Asn Lys Lys Tyr Leu Gly Leu Gln		
370	375	380
Met Leu Ser Leu Thr Val Pro Leu Ser Glu Glu Leu Lys Met His Tyr		
385	390	395
Pro Asp Phe Pro Asp Val Ser Ser Gly Val Tyr Val Cys Lys Val Val		
405	410	415
Glu Gly Thr Ala Ala Gln Ser Ser Gly Leu Arg Asp His Asp Val Ile		
420	425	430
Val Asn Ile Asn Gly Lys Pro Ile Thr Thr Thr Asp Val Val Lys		
435	440	445
Ala Leu Asp Ser Asp Ser Leu Ser Met Ala Val Leu Arg Gly Lys Asp		
450	455	460
Asn Leu Leu Leu Thr Val Ile Pro Glu Thr Ile Asn		
465	470	475

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Val Lys Val Thr Phe Asn Ser Ala Leu Ala Gln Lys Glu Ala Lys		
1	5	10
15		
Lys Asp Glu Pro Glu Ser Gly Glu Glu Ala Leu Ile Ile Pro Pro Asp		
20	25	30
Ala Val Ala Val Asp Cys Lys Asp Pro Asp Asp Val Val Pro Val Gly		
35	40	45
Gln Arg Arg Ala Trp Cys Trp Cys Met Cys Phe Gly Leu Ala Phe Met		
50	55	60
Leu Ala Gly Val Ile Leu Gly Gly Ala Tyr Leu Tyr Lys Tyr Phe Ala		
65	70	75
80		
Leu Gln Pro Asp Asp Val Tyr Tyr Cys Gly Ile Lys Tyr Ile Lys Asp		
85	90	95
Asp Val Ile Leu Asn Glu Pro Ser Ala Asp Ala Pro Ala Leu Tyr		
100	105	110
Gln Thr Ile Glu Glu Asn Ile Lys Ile Phe Glu Glu Glu Val Glu		

115	120	125
Phe Ile Ser Val Pro Val Pro Glu Phe Ala Asp Ser Asp Pro Ala Asn		
130	135	140
Ile Val His Asp Phe Asn Lys Lys Leu Thr Ala Tyr Leu Asp Leu Asn		
145	150	155
Leu Asp Lys Cys Tyr Val Ile Pro Leu Asn Thr Ser Ile Val Met Pro		160
165	170	175
Pro Arg Asn Leu Leu Glu Leu Ile Asn Ile Lys Ala Gly Thr Tyr		
180	185	190
Leu Pro Gln Ser Tyr Leu Ile His Glu His Met Val Ile Thr Asp Arg		
195	200	205
Ile Glu Asn Ile Asp His Leu Gly Phe Phe Ile Tyr Arg Leu Cys His		
210	215	220
Asp Lys Glu Thr Tyr Lys Leu Gln Arg Arg Glu Thr Ile Lys Gly Ile		
225	230	235
Gln Lys Arg Glu Ala Ser Asn Cys Phe Ala Ile Arg His Phe Glu Asn		240
245	250	255
Lys Phe Ala Val Glu Thr Leu Ile Cys Ser		
260	265	